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November 14, 2004, 15:03:41 ; Search time 79 Seconds (without alignments) 1552.980 Million cell updates/sec US-09-401-636-8 1856 1 BFHHHHHHTLSLPESGPVTI......HEALPGSRTLEKSLHYSAGN 342 1640122 5.1.6 Compugen Ltd. Total number of hits satisfying chosen parameters: 2002273 segs, 358729299 residues GenCore version Copyright (c) 1993 - 2004 OM protein - protein search, using sw model Gapop 10.0 , Gapext 0.5 **BLOSUM62** Title: Perfect score: Scoring table: Sequence: Searched: Run on:

Minimum DB seg length: 0 Maximum DB seg length: 342

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 23Sep04:*

1: geneseqp1980s:*
2: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Aab06205 Immunogen	Adf90025 Opossum-h	Adn00646 OSO prote	Aab06208 Immunogen	Aab03644 Opossum I	Aab06206 Immunogen	Adf90022 Opossum-r	Adn00643 ORO prote	Aab06202 Immunogen	Aab06201 Immunogen	Aao19667 Human IgE	Aau80286 Human IgE	Aau80285 Human IgE	Aau80284 Human IgE	Aar83559 Fc (epsilo	Aar75225 Human IgE	Aar77241 Human IgE	c i	Add25768 Binding d	Aau80289 Human IgE	Aay79994 Human imm		Aar85582 Fc(epsilo	N	Aay79995 Dog immun
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ALIGNMENTS

Immunogenic peptide consisting of opossum CH2, human CH3 and opossum CH4 Human; opossum; immunoglobulin B; IgE; vaccination; infection; allergy; asthma; eczema; immunogenic peptide. AAB06205 standard; protein; 342 AA 98US-0106652P. 99US-00401636. 99WO-SE001896. (revised)
(first entry) Didelphis virginiana. Homo sapiens. Chimeric. WO200025722-A2. 02-NOV-1998; 22-SEP-1999; 21-OCT-1999; 12-SEP-2003 22-NOV-2000 11-MAY-2000 AAB06205;

(RESI-) RESISTENTIA PHARM AB.

WPI; 2000-365342/31. Hellman LT;

Disclosure, Fig 2; 50pp; English.

Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin \boldsymbol{E} in mammals.

The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the human. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-2003 to standardise OS field)

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Gaps

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Best Local Similarity 100. Matches 342; Conservative

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Query Match Best Local Similarity

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Sequence 342

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host, e.g. CHO, cells. The invention provides methods and materials related to expressing chimeric IgE proteins. Mucleic acid vectors, host cells, and methods for producing chimeric IgE polypeptides are provided. When administered to a mammal, the chimeric polypeptides can reduce the IgE antibody effects of IgE-related diseases such as asthma, allergies
                                                                                                                                                                                                                             GVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRN
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                                                                                                                                                            Score 1786; DB 8;
Pred. No. 3.6e-140;
0; Mismatches 0;
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Local Similarity 99.4%;
les 334; Conservative
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                                                                                                                                                                                                                                                                           121 KCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHST
                                                                                                           1 EFHHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW
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                                                                          Gaps
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                                       Score 1856; DB 3;
Pred. No. 5.4e-146;
Mismatches 0;
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                                     100.0%; Sc
100.0%; Pr
:ive 0;
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antiasthmatic, dermatologica

virginiana

Chimeric. Didelphis ' Homo sapier

sapiens

WO2003096966-A2

27-NOV-2003.

(first entry)

26-FEB-2004

ADF90025 ADF90025;

RESULT :

Opossum-human chimeric

15-MAY-2003; 2003WO-IB002503 21-MAY-2002; 2002US-0382552P. (RESI-) RESISTENTIA PHARM AB.

WPI; 2004-042496/04. N-PSDB; ADF90024, ADF90023.

polypeptide

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Fuentes A,

Lundgren M,

us-09-401-636-8.closed.rag

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The present invention relates to a composition comprising a polypeptide and an aluminium compound, where the polypeptide comprises a self-IgB polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide:
ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or ADN00661. Administration of the composition to anamumal reduces the level of detectable free IgB in the mammal. The composition is useful for inducing an anti self-IgB antibody response in a mammal for treating or preventing allergies. The present sequence is an OSO procean, used to illustrate the invention. The OSO protein contains an opossum CH2 IgB domain followed by a human CH3 IgB domain followed by an opossum CH4 IgB
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                                                                                                                                                                                                                                                                                                                                                                Length 338;
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Best Local Similarity 99.4%; Pred. No. 3.6e-140;
Matches 334; Conservative 0; Mismatches 0;
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Chimeric.
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61 LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSR 120
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                                                                                                                                           The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the dog. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFHHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW
                                Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 RKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVY
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H
                                                                                                                                                                                                                                                                                                                                                                                                               88.6%; Score 1644.5; DB 3; Length 341; 88.0%; Pred. No. 2.2e-128; ive 17; Mismatches 23; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341
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                                                                                                        Disclosure, Fig 2; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.0%
Matches 301; Conservative
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WPI; 2000-365342/31
                                                                                                                                                                                                                                                                                                                                                                       Sequence 341 AA;
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22-SEP-1999;
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61 LVDGQBAENLFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSR 120
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                                                                                                                                                                                                                                                                                      The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the rat. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                  Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals.
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83.3%; Pred. No. 4.6e-122;
iive 20; Mismatches 36;
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              99WO-SE001896
                                                98US-0106652P.
99US-00401636.
                                                                                                    (RESI-) RESISTENTIA PHARM AB
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Didelphis virginiana.
                                                                                                                                                                        WPI; 2000-365342/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 341 AA;
                21-OCT-1999;
                                                02-NOV-1998;
22-SEP-1999;
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                                                                                                                                                                                    The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2, 3 and 4 of the opossum IgE. It was used to construct a number of immunogenic peptides which consisted of regions of IgE from different mammals, which appear to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema
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                                                                                                    Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin {\bf E} in mammals.
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Pred. No. 2.2e-123;
...trhes 28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Mismatches
                                                                                                                                                          Disclosure; Fig 1; 50pp; English
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85.1%;
RESISTENTIA PHARM AB
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         291; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    Sequence 341 AA;
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22-NOV-2000
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Chimeric.
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The present invention relates to a composition comprising a polypeptide and an aluminium compound, where the polypeptide comprises a self-IgE polypeptide sequence (e.g. a.m. ORO polypeptide or an OSO polypeptide. ADN06643, ADN06646, ADN06650, ADN06650 or level of the composition of the composition to a mammal reduces the level of detectable free IgE in the mammal. The composition is useful for inducing an anti self-IgE antibody response in a mammal for treating or preventing allergies. The present sequence is an ORO protein, used to illustrate the invention. The ORO protein, used to domain followed by a rat CH3 IgE domain followed by an opossum CH4 IgE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKL--PGKRLAPEVYMLPPSP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EETGTTRIVTCLIRGFYPSEISVOWLFNNEEDHTGHHTTTRPOKDHGTDPSFFLYSRMLV 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 NIFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRRCSDDEPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 TLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAE
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                                                                                                                                                                                                                                                                                                                                                                                                            New composition comprising a self-IgE polypeptide and an aluminum compound, useful for inducing an anti self-IgE antibody response in mammal for treating or preventing allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8; Length 337;
                                     ORO; OSO; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.7%; Score 1498.5; DB 8; 82.4%; Pred. No. 3.1e-116; ive 20; Mismatches 36;
                                                                                                                                                                                                                                                                                                                    Gansson A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.4%; EL.
                                     Antiallergic; Vaccine; self-IgE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Fig 4; 102pp; English
                                                                                                                                                                                                2003WO-IB003075.
                                                                                                                                                                                                                                   05-SEP-2002; 2002US-0408648P.
                                                                                                                                                                                                                                                                            (RESI-) RESISTENTIA PHARM AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity o...
Matches 277; Conservative
                                                                                                                                                                                                                                                                                                                  Hellman LT, Persson S,
ID 3.
                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-248376/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
SEO
                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADNO0642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 337 AA;
                                                                                                                 WO2004022094-A1
                                                                                                                                                                                             02-JUN-2003;
protein,
                                                                                                                                                          18-MAR-2004
                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
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ID AAB06202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
ORO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the protein sequence of an opossum CH2-rat CH3-opossum CH4 (ORO) chimeric IgE polypeptide. A vector comprising a nucleic acid encoding ORO can be used for recombinant production of this chimeric IgE in host, e.g. CHO, cells. The invention provides methods and materials related to expressing chimeric IgE proteins. Nucleic acid vectors, host cells, and methods for producing chimeric IgE polypeptides are provided. When administered to a mammal, the chimeric polypeptides can reduce the IgE antibody effects of IgE-related diseases such as asthma, allergies and eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EETGTTRTVTCLIRGFYPSEISVQWLFNNEEDHIGHHTTTRPQKDHGTDPSFFLYSRMLV 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BETGTTRIVTCLIRGFYPSELSVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                  New host cell comprising a nucleic acid vector comprising a cytomegalovirus promoter, an Ig leader sequence, an insert sequence or SV40 late polyadenylation sequence, useful in producing a chimeric IgE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIOLLCLVSGFSPAKVHVTWLVDGQEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRKCADSNPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKL--PGKRLAPEVYMLPPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLSLPESGPVT1IPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 337;
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w
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80.7%; Score 1498.5; DB 8;
Best Local Similarity 82.4%; Pred. No. 3.1e-116;
Matches 277; Conservative 20; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID NO 3; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 337
                                                                                                                                                       21-MAY-2002; 2002US-0382552P
                                                                                                                                                                                             (RESI-) RESISTENTIA PHARM AB
                                                                                                                    15-MAY-2003; 2003WO-IB002503
                                                                                                                                                                                                                                                                         WPI; 2004-042496/04.
N-PSDB; ADF90020, ADF90021
                                                                                                                                                                                                                                      Fuentes A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADN00643 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 337 AA;
                                     WO2003096966-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-2004
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                                                                         27-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADN00643;
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dd ò 셤 δ g 8 g ò d ò 셤

128 122

68 62

<u>ب</u>

Indels

181

SYSYEX

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238 VYMLPPSPEETXTTRTVTCLIRGFYPSEISVQWLFXXEEDHTGHTTTRPQKDHGTDXSF 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opsosum IgE and the heavy chain constant region 3 created from a combination of the one from the rat and the opesaum. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur. pollen and food allergies and eczema. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                  Immunogenic peptide consisting of opossum CH2, CH4 and rat/opossum CH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals.
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                                                                                                                                                                                                                                                                                                                                                                                         Rat, opossum, immunoglobulin E, IgE, vaccination, infection, allergy, asthma, eczema, immunogenic peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 74.1%; Score 1375; DB 3; Length 3 Local Similarity 76.6%; Pred. No. 6e-106; les 262; Conservative 23; Mismatches 55; Indels
                                                                                    FLYSRMLVHKSIWEKGHLVTCRVVHEALPGSRTLEKSLHYSAG 340
                                                              FLYSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Xaa=unknown'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                         AAB06201 standard; protein; 342 AA.
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/label= OTHER
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                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Didelphis virginiana.
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22-SEP-1999;
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22-NOV-2000
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                                                                                                                                                                                                                                                 AAB06201;
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                                                                                                      298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 VYMLPPSPEETGTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 KCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHST 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 XQWYTKHHHHATTXITSILPVVXKDWIEGYXYQXIXDHPHPIKXXVPSITRLPGKRLAPX 237
                                                                                                                             Immunogenic peptide consisting of opossum CH2, mouse CH3 and opossum CH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                  Mouse, opossum; immunoglobulin E; IgE; vaccination; infection; allergy; asthma; eczema; immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the mouse. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against becterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                          /note= "Xaa=unknown"
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 2; 50pp; English
                                                                                                                                                                                                                                                                                                                                   1. .341
/label= OTHER
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99US-00401636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 76.7
Matches 263; Conservative
                                                                 (revised)
                                                                                                                                                                                                                               Didelphis virginiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-365342/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 341 AA;
                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                 WO200025722-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-NOV-1998;
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                                                              12-SEP-2003
22-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hellman LT;
                                                                                                                                                                                                                                                     Mus sp.
Chimeric.
                       AAB06202;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fusion molecules comprising polypeptide sequences that bind to IgG inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.
                                                     KCADSNPRGVSAYLSRPSPFDLF1RKSPT1TCLVVDLAPSKGTVNLTWSRASGKPVNHST
                                                                                                                                                                                                                        YMLPPSPEETXTTRTVTCLIRGFYPSEISVQWLFXXEEDHTGHHTTTRPQKDHGTDXSFF
181 RKEBKQR-NGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEV
                                                                                                                                                       SLVVKEXYHGTFTXTSHLPVETDDWIEGXTYTXXLESPDMIVILIPTISALPGKRLAPXV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; IgE; immunoglobulin E; immunotherapy; immune disease;
Reopsilon receptor; autoimmune disease; constrant region; heavy
antiasthmatic; antiallergic; antiinflammatory; dermatological;
antiarthritic; antirheumatic; antiidiabetic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human IgB heavy chain constant region CH2-CH3-CH4 portion.
                                                                                                                                                                                                                                                               LYSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
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                                                                                                                                                                                                                                                                                                                                                                                   AA019667 standard; protein; 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic; antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE; vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis; heavy chân C domain.
or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human IgE heavy chain constant region CH2-CH3-CH4 portion
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                                                                                                                                                    3 PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMD---VDLSTASTTQE
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                                                                                 DB 6;
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                                                                                        , Pred. No. 5.7e-78;
41; Mismatches 73
                                                                               56.0%; Score 1038.5; 62.4%; Pred. No. 5.7e-
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15-SEP-2000; 2000US-0232831P.
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                                                      Sequence 320 AA;
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Matches 201;
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15-SEP-2000; 2000US-0232831P
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N-PSDB; ABK51133.
                         (PHAR-) PHARMEXA AS.
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                     This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell pricope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCS) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C2-C3-C4 domains optimised for expression in an B. Coli system, this sequence was used to create the epitopes of the invention
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                                                                                                                                                                                                                                                                     Gaps
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 Disclosure; Page 112-113; 151pp; English
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62.4%;
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This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from igE, and T helper cell epitope (TH epitope) which is foreign to the animal. by antigen presenting cells (APCS) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human system, this sequence was used to create the epitopes of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 KDWIEGETYQCRVTHPHLPRALMRSTIKTSGPRAAPEVYAF-ATPEWPGSRDKRTLACLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5;
Gautam A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.0%; Score 1038.5; DB 962.4%; Pred. No. 5.8e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Mismatches
                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 108-110; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human IgE heavy chain C2-C3-C4 domains.
Voldborg B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVVHEALPGSRTLEKSLHYSAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAVHEAASPSQTVQRAVSVNPG 322
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Von Hoegen
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64

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142 124 202

GQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRKCADSNPRGVSAYLSRPSPFD

319

184

243

260

RVVHEALPGSRTLEKSLHYSAG 341

320 301

259 242

183

LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT RDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPEETGT--TRTVTCLI RGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKSIWEKGNLVTC

LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT

201

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This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IGE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IGE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen the surface (TH epitope) which is foreign to the animal, by antigen the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IGE in the animal, which is useful for downregulating autologous IGE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IGE heavy chain C2-C3-C4 domains used to create the epitopes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inducing immune response against autologous immunoglobulin B in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin.
vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
heavy chain C domain.
                                                                                                                                                                                                                                                                                   210. 218
210. 218
210. 218
212. 215
//note= "Linker between domains C3 and C4"
216. 317
                                                                                                                                                                  C3 ª
                                                                                                                   100. .114.
/note= "Epitope including C2C3 linker"
104. .111
/note= "Linker between domains C2 and C
                                                                                            8. .103
/note= "IgE heavy chain C2 domain"
                                                                                                                                                                            112. .211
/label= 19E heavy chain C3 domain
139. .145
/note= "Epitope in BC loop"
167. .175
                                                                                                                                                                                                                                                                                                                                                                        "IgE heavy chain C4 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gautam A;
                                                                                                                                                                                                                                                  /note= "Epitope in DE loop"
196. .206
                                                                                                                                                                                                                                                                                /note= "Epitope in FG loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 105-106; 151pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Voldborg
                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000; 2000DK-0001326.
15-SEP-2000; 2000US-0232831P.
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                                                                                                                                                                                                                                                                                                                                                           216. .3:
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PHAR-) PHARMEXA AS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    WO200220038-A2
                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-2002
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                                                                                         Domain
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                                                                                                                                                                                                                                                                                                                                                           Domain
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Fc(epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter; constant heavy region; E.coli; glycosylation; antigenic; immunogenic; histamine; anti-allergenic; vaccine; immune response.

CH2'-CH4 protein sequence.

(first entry)

06-MAR-1996

AAR83559;

Fc(epsilon)

Ä

AAR83559 standard; protein; 324

AAR83559

(INMR) PASTEUR MERIEUX SERUMS & VACCINS.

94FR-00000846. 94FR-00000846

26-JAN-1994;

26-JAN-1994;

FR2715304-A1

Synthetic

28-JUL-1995.

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The amino acid sequence of the Fc(epsilon) CH2'-CH4 fragment covering amino acids 226-547. The DNA sequence was isolated from a human myeloma 266-547. The DNA sequence was isolated from a human myeloma cases. CDNA contains of the N-terminus of INT-10 index control of the tryptophan promoter. The resultent protein pwT211 under control of the tryptophan promoter. The resultent protein pwT211 under contains some non-Fc amino acids. These were removed by replacing their coding sequence with a bicistronic linker. The resultant construct encodes the Fc(epsilon) constant heavy region from amino acids 226-547. When it is expressed in E.coli, the protein produced is a non-unmasks new antigenic sites thus rendering the Pattern of glycosylation unmasks new antigenic sites thus rendering the Ffragment immunogenic and able to induce antibodies that recognise native IgE but do not form histamine-releasing complexes. The Fc fragments can be used in anti-allergenic vaccines to modulate the intensity of immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain epitope(s) not present in native IgE, also derived antibodies for treating or preventing allergies, inflammatory immune disease, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 32-33; 44pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                  Panero MJM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-265243/35.
N-PSDB; AAT01865.
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4.

Gaps

7;

Indels

DB 5; Length 323;

Query Match 56.0%; Score 1038.5; DB 5; Best Local Similarity 62.4%; Pred. No. 5.8e-78; Matches 201; Conservative 41; Mismatches 73;

à

81 63

PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMD--VDLSTASTTQE 22 PPIVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAENLFPYTTRPKREG

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82 GOTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRKCADSNPRGVSAYLSRPSPFD 141
                                                                                                                                                           260 RGFYPSEISVOWLFNNEEDHTGHHTTTRPOKDHGTDPSFFLYSRMLVNKSIWEKGNLVTC 319
                                                                                                                                                                                                                                                                                                                244 QNFMPEDISVQWLHNBVQLPDARHSTTQPRKTKGS--GFFVFSRLEVTRAEWEQKDEFIC 301
                                                                                     22 PPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAENLFPYTTRPKREG 81
                                                                                                      7 PPTVKILQSSCDGGGHPPPTIQLLCLVSGYTPGTINITWLEDGQVMD--VDLSTASTTQE 64
                                                              Gaps
                                                             7;
                                 Query Match 56.0%; Score 1038.5; DB 2; Length 324; Best Local Similarity 62.4%; Pred. No. 5.8e-78; Matches 201; Conservative 41; Mismatches 73; Indels 7;
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            Sequence 324 AA;
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Search completed: November 14, 2004, 15:06:52 Job time : 81 secs

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November 14, 2004, 15:06:56 ; Search time 79 Seconds (without alignments) 1531.723 Million cell updates/sec
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1856
I EFHHHHHTTLSLPESGPVTI......HEALPGSRTLEKSLHYSAGN 342
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1: /cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1568699 seqs, 353819137 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 342
                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 8, Appli	Sequence 8, Appli	.~	Sequence 6, Appli	Sequence 6, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Seguence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 9, Appli	Sequence 9, Appli
ID	US-09-401-636-8	US-10-176-664-8	US-10-673-594-8	US-10-438-794-6	US-10-453-915-6	US-09-401-636-11	US-10-176-664-11	US-10-673-594-11	US-09-401-636-3	US-10-176-664-3	US-10-673-594-3	US-09-401-636-9	US-10-176-664-9
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15 US-10-673-594-9	9 US-09-401-636-4	0-176-6	5 US-10-673-59	-401-63	4 US-10-176-66	3-5	US-09-401-636-	US-10-176-664-	US-10-673-594-	US-10-438-794-	1-453-91	US-09-847-208-	4 US-10-000-439-	US-09-949-	-949-375A	US-09-949-37	US-10-363-95	-363-954A-	1-363-954	-401)-176-66	14 US-10-207-655-329	15 US-10-673-594-1	US-09-949-375A-	0-363-9	US-09-949-37	6 US-10-363-95	6 US-10-704-4	US-09-809-746	809-715-	16 US-10-704-406-2
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ALIGNMENTS

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RESULT 1 US-09-401-636-8	; Sequence 8, Application US/09401636 ; Patent No. US20010038843A1	; GENERAL INFORMATION: ; APPLICANT: Hellman, Lars T.	; TITLE OF INVENTION: ENHANCED VACCINES	; FILE REFERENCE: 10223/006001 ; CHERENT APPLICATION NUMBER: HS/09/401.636	; PRIOR APPLICATION NUMBER: US 60/106,652	; PRIOR FILING DATE: 1998-11-02 ; NUMBER OF SEO ID NOS: 11	; SOFTWARE: FastSEQ for Windows Version 4.0	; SEQ ID NO 8	TYPE: PRI	ORGANISM: Artificial Sequence	; FEATURE: OTHER INFORMATION: Synthetically generated proteins	US-09-401-636-8	Query Match 100.0%; Score 1856; DB 9; Length 342; Best Local Similarity 100.0%; Pred. No. 1.5e-139;	vative 0;	Qy 1 BFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW 6	Db 1 EFHHHHHHHLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW	Qy 61 LVDGQEAENLFPYTTRFKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSR 1	Db 61 LVDGQEAENLFFYTTRFKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSR 1	QY 121 KCADSNPRGVSAYLSRPSPFDLFIRKSPFITCLVVDLAPSKGTVNLTWSRASGKPVNHST 1

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FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/10/673,594
CURRENT FILING DATE: 10395-09-29
PRIOR PLING DATE: 1999-09-22
PRIOR PLING DATE: 1999-09-22
PRIOR PLING DATE: 1999-09-22
PRIOR PILING DATE: 1998-11-02
NUMBER: OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                          241 MLPPSPEETGTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFL 300
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  KCADSNPRGVSAYLSRPSPPDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHST 180
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                                                                                                                                                                                                                                                       301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
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Publication No. US20030031663A1

GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
APPLICANT: Hellman, Lars T.
TITLE OF INVERTION: ENHANCED VACCINES
FILE REFERENCE: 10223/00601
CURRENT APPLICATION NUMBER: US/10/176,664
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR PILING DATE: 1999-09-22
PRIOR PILING DATE: 1999-09-22
PRIOR PILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 342
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US-10-673-594-8
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Publication No. US20040038395A1

GENERAL INFORMATION:
APPLICANT: LUNGGREW, Mate
APPLICANT: FUENTES, Alexis
APPLICANT: CHENTES, Alexis
APPLICANT: MAGNUSSON, Ann-Christin
TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
FILE REFRENCE: 10223-017001
CURRENT APPLICATION NUMBER: US/10/438,794
CURRENT FILING DATE: 2003-05-15
PRIOR APPLICATION NUMBER: US 60/382,552
PRIOR APPLICATION NUMBER: US 60/382,552
MUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                            Query Match 100.0%; Score 1856; DB 15; Length 342; Best Local Similarity 100.0%; Pred. No. 1.5e-139; Matches 342; Conservative 0; Mismatches 0; Indels 0;
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FEATURE: OTHER INFORMATION: Synthetically generated proteins US-10-673-594-8
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DB 15; Length 338;

96.2%; Score 1786;

Query Match

Sequence 8, Application US/10673594 Publication No. US20040076625A1 GENERAL INFORMATION:

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61 LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSR 120
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243 EETGTTRITVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLV 302
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                                                                                             303 NKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 338
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88.6%; Score 1644.5; DB 9;
Best Local Similarity 88.0%; Pred. No. 1.1e-122;
Matches 301; Conservative 17; Mismatches 23;
                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
RIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 11
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TITLE OF INVENTION: EMFANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/10/176,664
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
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                                                                                                                                                                                                            ; Sequence 11, Application US/09401636; Patent No. US20010038843A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-09-401-636-11
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US-10-176-664-11
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Pred. No. 5.7e-134;
0; Mismatches 0;
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US-10-453-915-6
Sequence 6, Application US/10453915
Publication No. US20040054146A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
APPLICANT: Persson, Stefan
APPLICANT: Jansson, Asa
TITLE REPREBNCE: 10223-008001
CURRENT APPLICATION NUMBER: US/10/453,915
CURRENT FILING DATE: 2003-06-05
PRIOR FILING DATE: 2003-06-05
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 6
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99.48;
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Best Local Similarity 99.4
Matches 334; Conservative
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85.4%; Pred. No. 3.8e-118;
iive 21; Mismatches 28;
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TITLE OF INVENTION: ENHANCED VACCINES
FILE REPERENCE: 1022/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR PELING DATE: 1996-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SED ID NO 3
LENGTH: 341
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US-10-176-664-3
; Sequence 3, Application US/10176664
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ORGANISM: Artificial Sequence
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Matches 292; Conservative
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                                                                                                                                                                                                        88.6%; Score 1644.5; DB 14; Lengt
88.0%; Pred. No. 1.1e-122;
.ive 17; Mismatches 23; Indels
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                                                                                                                                    ; OTHER INFORMATION: Synthetically generated proteins US-10-176-664-11
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Pred. No. 1.1e-122;
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Publication No. US20040076625A1
GENERAL INPORMATION:
FILE REPERENCE 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT PILING DATE: 2003-09-29
PRIOR PILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
INDETH: 341
TYPE: PRT
PRIOR PRING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
TYPE: PRT
    NUMBER OF SEQ ID NOS: 11
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 341
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Best Local Similarity 88.0%;
Matches 301; Conservative 17
                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 88.03
Matches 301; Conservative
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US-10-673-594-11
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 285; Conserv
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US-09-401-636-9
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                                                                                                                                                                                                                                                                                                                                                                                               Length 341;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 85.5%; Score 1587.5; DB 14; Lengt Best Local Similarity 85.4%; Pred. No. 3.8e-118; Matches 292; Conservative 21; Mismatches 28; Indels
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Publication No. US20040076625A1
GENERAL INFORMATION:
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/10/673,594
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR PILING DATE: 1999-09-22
PRIOR PILING DATE: 1999-09-22
PRIOR PILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
           GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TILE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,664
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1999-01-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NOS: 11
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Publication No. US20030031663A1
                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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Query Match 85.5%; Score 1587.5; DB 15; Lengt
Best Local Similarity 85.4%; Pred. No. 3.8e-118;
Matches 292; Conservative 21; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
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Patent No. US20010038843A1
SERNEAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR PLING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9.
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FastSEQ for Windows Version 4.0
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SEQ ID NO 9
LENGTH: 341
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                                                                                                    TYPE: PRT
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240 MLPPSPEETGTTRIVICLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFL 299
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84.5%; Score 1568.5; DB 14
Best Local Similarity 83.3%; Pred. No. 1.2e-116;
Matches 285; Conservative 20; Mismatches 36;
                                                                                                                                                                                                                                            TITLE OF INVENTION: BAILAND VACCINES
TITLE BEFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/10/176,664
CURRENT FILING DATE: 2002-06-19
RRIOR APPLICATION NUMBER: US/09/401,636
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: ASSOCIATION US
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                                                                                                                                                                                   Sequence 9, Application US/10176664; Publication No. US20030031663A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-10-176-664-9
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US-10-673-594-9
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Best Local Similarity 82.7%; Pred. No. 1.9e-115;
Matches 283; Conservative 21; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                      84.5%; Score 1568.5; DB 15; Lengt
83.3%; Pred. No. 1.2e-116;
iive 20; Mismatches 36; Indels
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                                                                                                                                                                                                                   FEATURE: , OTHER INFORMATION: Synthetically generated proteins US-10-673-594-9
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Patent No. US20010038843A1
GENERAL INFORMATION:
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR SPOINT SILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PASISEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.33
Matches 285, Conservative
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OM protein - protein search, using sw model

November 14, 2004, 15:03:41 ; Search time 24 Seconds (without alignments) 1371.089 Million cell updates/sec Run on:

US-09-401-636-8 1856 1 EFHHHHHHTLSLPESGPVTI.......HEALPGSRTLEKSLHYSAGN 342 Perfect score: Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 342

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dł				
Result		Query				
No.	Score	Match	Length	DB	QI	Description
н	9		N	П	GZHU	g gamma-2
7	476	'n.	N	Н	G4HU	g gamma-4 cha
٣	473.5	25.5	\sim	~	147161	g gamma 3
4	9	'n	\sim	~	4716	g gamma 2b cha
5	465	25.1	\sim	7	147159	g gamma 2a
ø	463.5	'n	328	0	I47158	amma 1 c
7	454	4.	3	Н	GHHU	g gamma-1
œ	447	4,	~	(1	147162	g gamma 4
6	443.5	ω.	N	~	PS0019	g gamma-2a
	7	23.6	C	Н	GHRB	g gamma ch
11	436.5	ω.	N	7	PS0017	g gamma-
12	428	ω.	N	7	S00847	σ
13	424.5	ų.	N	Н	G2GP	g gamma-2 chai
14	N	ď.	m	Н	G2MSAB	g gamma-
15		22.5	0	7	C30554	b
16	415.5	∾.	$^{\circ}$	H	G1MS	g gamma-1
17	413	'n	N	7	806611	g gamma-2
18	402.5	21.7	n	4	831866	ים
19	401.5	ä	ထ	Н	G3HUWI	ים
20	S	ä	$^{\circ}$	Н	G3MSC	g gamma-3
21	395.5	ä	33	~	GZMSA	סו
22	ŝ	。	. 23	~	PT0207	b
23	œ	。	33	N	PS0018	ים ים
24	ö	20.0	34	~	I56230	g alpha-2 cha
25	69	9.	34	N	2236	galp
26	359.5	6	34	~	A2HU	g alpha-2 chain
27	43.	ω.	m	N	ø	galp
28	18	٠	34	N	4	g alpha chain C
29	0		18	(1	4673	g

Ig alpha chain C r	Ig alpha chain C r	Ig alpha chain C r	Ig gamma-1 chain C	IgE chain C4 regio	chain C4	Ig alpha-2 chain C	chair	alpha chain	Ig heavy chain V-I	IgE chain C3 regio	Ig heavy chain VHI	Ig gamma chain (cl	Ig heavy chain Cr	Ig upsilon chain -	Ig epsilon chain C
w	4	ω.	9	7	7	0	9		0	0	0	0	8	89	5.
80927	80926	809275	S1423	I6873	I6872	C22360	168726	AHRB	A36040	I68730	S6934	80305	S1232	S4314	PH1215
2 S0927	2 80926	2 80927	2 S1423	2 I6873	2 I6872	2 C2236	2 I6872	1 AHRB		2 I6873					2 PH121
7	7	335 2 80927	(1	N	7	0	C)	н	7	8	7	7	7	7	α
338 2	339 2	~	152 2	115 2	115 2	220 2	107 2	299 1	218 2	107 2	249 2	228 2	244 2	111 2	227 2
338 2	16.1 339 2	335 2	15.4 152 2	15.2 115 2	15.1 115 2	14.7 220 2	14.1 107 2	299 1	13.8 218 2	107 2	13.3 249 2	13.0 228 2	12.7 244 2	11.8 111 2	11.5 227 2

ALIGNMENTS

н	
SULT	5

Iggamma-2 chain C region - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: A33906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
R;Ellison, J.; Hood, L.
A;Tille: Linkage and sequence homology of two human immunoglobulin gamma heavy chain co A;Reference number: A93906; MUID:82197621; PMID:6804948

A, Molecule type: DNA
A, Residues: 1-326 (ELL)
A, Residues: 1-326 (ELL)
A, Residues: 1-326 (ELL)
A, Note: Lys-326 is probably removed posttranslationally
A, Note: Lys-326 is probably removed posttranslationally
A, Note: Lys-326 is probably removed posttranslationally
B, Manag, A.C.; Tung, B.; Fudenberg, H.H.
B, Mang, A.C.; Tung, B.; Fudenberg, H.H.
B, Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
A, Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
A, Reference number: A92809; MUID: 81007873; PMID: 6774012
A, Rocession: A92809
A, Rocession: A92809
A, Residues: 1-19, 'Q', 21-57, 'Z', '59, 'A', 61-193, 'D', 195-325 <WAN>
A, Note: Trp-156 is at or near the complement-binding site
R, Connell J, G.E.; Parr, D.M.; Hefmann, T.
Can. J. Biochem: 57, 758-767, 1979
A, Title: The amino acid sequences of the three heavy chain constant region domains of a A, Title: The amino acid sequences of the three heavy chain constant region domains of A, Contents: myeloma protein Zie
A, Accession: A0752.

A Molecule type: protein

A, Molecule type: protein

A, Residues: 1-24, E., 26-57, EV', 60-85,132-171, 'ZZZ',175,'B',177-193,'D',195-196,'Q',198

A, Note: this sequence has since been revised

R, Hofmann, T.; Parr, D.M.

R, Hofmann, T.; Parr, D.M.

A) I, Immunol. 16, 923-925, 1979

A, Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin

A, Reference number: A93132; MUID:80114419; PMID:118920

A; Contents: Zie A; Accession: A93132

residues 25, 59, 60, and 264-268 that shown in having 60-Ala and in the amidat A Molecule type: protein
A Mesidues: 238-275 <4D0PR;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A945931
A;Contents: annotation; Zie, revisions to
A;Note: the revised sequence differs from

Rifilstein, C.; Frangione, B. Blochem. J. 121, 217-225, 1971 A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2. A;Reference number: A90253; MUID:72033500; PMID:4940472 A;Contents: annotation; myeloma protein Sa, disulfide bonds

N

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Amap position: 14932.33-14932.33

Anterons: 99/1; 111/1; 221/1

Anterons: 99/1; 111/1; 221/1

Anterons: 99/1; 111/1; 221/1

Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology

C; Superfamily: immunoglobulin homology < IMI>
F; 20-10/Region: hinge
F; 39-110/Region: hinge
F; 39-110/Region: immunoglobulin homology < IMI>
F; 240-307/Domain: immunoglobulin homology < IMI
F; 240-307/Domain: immunoglobulin homology < IMI
F; 240-307/Domain: immunoglobulin homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R,Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A,Title: Five putative subclasses of swine 1gG identified from the cDNA sequences of
A,Reference number: 147158; MUID:95015845; PMID:7930579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLP 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 KDILMISRIPEVICVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIRGEYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKSIWEKGNLV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 LVKGFYPSDIAVEWESNGQPEN--NYKTTPPVLD--SDGSFFLYSRLTVDKSRWQEGNVF 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 RDTSGPNVALGCLASSYFPEPVTMTWNSGALTSG---VHTFPSVLQP----SGLYSLSSM 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig gamma 3 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb.1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 RGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPKREGGQTFSLQSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 RGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPKREGGQTFSLQSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG---VHTFPAVL----QSSGLYSLSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPEE-TGTTRTVTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: U03781; NID: 9433127; PIDN: AAA52219.1; PID: 9433128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.6%; Score 476; DB 1; Length 327; 35.8%; Pred. No. 4.1e-28; cive 57; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNITOGOWMSSNTYTCHVKHNGSIFEDSSRKCADSNP-
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A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-328 <KAC>
                                                OMIM:147130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCRVVHEALPGSRTLEKSLHYSAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 SCSVMHEALHNHYT-QKSLSLSLG 326
                                                    A; Cross-references: GDB:119340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity ....
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Riprangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A.Title: Structural studies of immunoglobulin G.
A.Fitle: Structural studies of immunoglobulin G.
A.Fitle: Structural studies of immunoglobulin G.
A.Gontents: annotation; Sa, disulfide bonds
C.Gontents: annotation; Sa, disulfide bonds
C.Gontents: annotation; Sa, Gullide bonds
A.Gontents: annotation; Sa, Gullide bonds
A.Gontents: An immunoglobulin heterotetramer subunit consists of two identical light (kap A.Gontes: An immunoglobulin heterotetramer subunit consists of two identical light (kap C.Gonter An immunoglobulin heterotetramer; immunoglobulin heterotetramer; immunoglobulin homology
C.Seywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology < IMI>
F.20-88/Domain: immunoglobulin homology < IMI>
F.33-202/Domain: immunoglobulin homology < IMI>
F.33-306/Domain: immunoglobulin homology < IMI>
F.31-303/Bollide bonds: interchain (to light chain) #status experimental
F.102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F.105/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Using gamma-4 chain C region - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90933, A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA J. 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Title: DNA
A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Corss-references: UNIPROT:P01861
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
B;Onchem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant r
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 RSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG---VHTFPAVL----QSSGLYSLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 D-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 GTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPEE-TGTTRTVTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 RGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPKREGGQTFSLQSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.2%; Score 486.5; DB 1; Length 326; 36.2%; Pred. No. 6.7e-29; ive 57; Mismatches 120; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 CRVVHEALPGSRTLEKSLHYSAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 CSVMHEALHNHYT-QKSLSLSPG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 36.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
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---LVDGQEAENLFPYTTRP

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Ig gamma 1 chain constant region - pig (fragment)
(j.Species: Sus scrofa donnestica (donnestic pig)
(j.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
(j.Accession: 147158
(R.Kaskovics, I.; Sun, J.; Butler, J.E.
(j.Tumunol, 15), 3565-3573, 1994
(j.Tumunol, 15), 3565-3573
(j.Tumunol, 15), 356
Ig gamma 2a chain constant region - pig (fragment)

C;Species: Sus scrofa domestica pig)

C;Accession: 147159

R;Accession: 147159

R;Accession: 147159

R;Accession: 153, 356-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Stetus: preliminary; translated from GB/EMBL/DDBJ

A;Accession: 147159

A;Cosperation: 147159

C;Genetics: 147159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 RNGTLIVISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTIKLPGKRLAPEVYMLPPSP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 RGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQ 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EETGTTR-TVTCLIRGEYPSEISVOWLFNNEEDHTGHHTTTRPOKDHGTDPSFFLYSRML 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 IQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNITQGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 PSVYPLAPCSRDTSG---PNVALGCLASSYFPEPVTVTWNSGALSSG---VHTFPSVLQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SGLYSLSSMVTVPASS-LSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.0%; Score 463.5; DB 2; Length 328;
.larity 33.9%; Pred. No. 3.5e-27;
Conservative 58; Mismatches 124; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: 1gG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||:||: | : | : | ||||| | :||: | VDKASWQGGGIFQCAVMHEALHNHYT-QKSISKTPG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
25.1%; Score 465; DB 2; L
Best Local Similarity 33.0%; Pred. No. 2.7e-27;
Matches 111; Conservative 58; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 PPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Sus screfa domestica (domestic pig)
C.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C.Accession: 147160
R.Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A.Fitle: Five putative subclasses of swine IgG identified from the cDNA sequence
A.Fitle: Five putative subclasses of swine IgG identified from the cDNA sequence
A.Facession: 147160
A.Facession:
                                               140
                                                                                                                                                                                                                                                                                                                                                   258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 NPRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPEETGTIR-TVICLIRGFYPSEISVQWLFNNEEDHIGHHITTRPQKDHGTDPSFFLYSR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma 2b chain constant region - pig (fragment)
Species: Sus scrofa domestica (domestic pig)
Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 RPKREGGQTFSLQSEVNITQGQMMSSNTYTCHVKHNGSIFEDSSRK------CADS
                                                                                               PKTAPLVYPLAPCG-RDTSGPNVALGCLASSYFPEPVTVTWNSGALTSG----VHTFPSVL
                                                   -CADSNPRGVSAYLSRPSPF
                                                                                                                                                                                                   D-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPV
                                                                                                                                                                                                                                                                                                                                                   200 GTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPEETGTTR-TVTCL
                                                                                                                                                                                                                                                                                                                                                                                               KORNGTLIVISTLPVGTRDWIEGETYOCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPP
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Larity 32.8%; Pred. No. 1.6e-27;
Conservative 61; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327
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FSVDKASWQGGGIFQCAVMHEALHNHYT-QKSISKTPG
                                                   VNITQGQWMSSNTYTCHVKHNGSIFEDSSRK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAVMHEALHNHYT-OKSISKTOG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRVVHEALPGSRTLEKSLHYSAG 341
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Best Local Similarity
Matches 111; Conserv
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Gaps

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976 A.Title: Die Primerstruktur eines monoklonalen Iggl-Immunglobulins (Myelomprotein	igen Primaerstruktur. A;Reference number: A91668; MUID:77070269; PMID:826475 A;Contents: myeloma protein Nie	79 4t	K;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hischmann, N. Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983 A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins 54 A;Reference number: A91723; MUID:83289131; PMID:6884994	A; Contents: myeloma protein KOL; disulfide bonds A; Accession: A91723 A; Molecule type: protein A; Mesidues: 1-96, K*, 98-117, D*, 199-238, E*, 240, M*, 242-266, D*, 268-271, D* A; Mesidues: 1-96, R*, 98-194, D*, 199-238, Meridua, 1) markers	A;NOCE: LIES SQUENCE AND STRUCT A	A;Contents: annotation; disulfide bonds R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976 A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 enbromide cleavage products, and the disulfide bridges. A;Reference number: A91667; MUD:77070267; PMID:1002129 A;Contents: annotation; disulfide bonds	A;Gene: GDB:IGHG1 A;Gene: GDB:IGHG1 A;Cross-references: GDB:120085; CMIM:147100 A;Map position: 14922.33-14932.33 A;Introns: 99/1; 114/1; 224/1 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light C;Complex: An immunoglobulin heterotetramer subunit sassociate in C;Complex: An immunoglobulin C;Complex: An immunoglobulin C;Complex: An immunoglobulin C;Complex: An immunoglobulin heterotetramer; immunoglobulin	F:20-85/Domain: immunoglobulin homology <im1> F;137-206/Domain: immunoglobulin homology <im2> F;137-206/Domain: immunoglobulin homology <im2> F;27-83,144-204,250-308/Disulfide bonds: #status experimental F;103/Disulfide bonds: interchain (to light chain) #status experimental F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental F:180/Binding site: carbohvdrate (Asp) (covalent) #status experimental</im2></im2></im1>	ution of a	Qy 22 PPTVKLFHSGDPRGDAHSTIQLCLVSGFSPAKVHVTWLVDGQEAENLFPYTTRP	cy 78 KREGGGTFSLQSEVNITQGGWMSSNTYTCHVKHNGSIFEDSSRKC	Qy 124 DSNPRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRK	G.M. Db acid seque	38,'E',240, Qy 302
23 VALGCLASSYFPEPVTVTWNSGALTSGVHTFPSVLQPSGLYSLSSMVTVPASS 75	98 WMSSNTYTCHVKGNGSIFEDSSRKCADSNPRGVSAYLSRPSPFD-LFIRK 14	147 SPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEBKQRNGTLIVTSTLÞVGTRDWIE 20 	207 GETYQCRVTHPHLPRALMRSTTKLPGKRLAPBVYMLPPSPEETGTTR-TVTCLIRGFYPS 26	266 EISYQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKSIWEKGNLVTCRVVHEA 32 : :	326 LPGSRTLEKSLHYSAG 341 : : : 313 LHNHYT-QKSISKTQG 327	chain C region - human Homo sapiens (man) -Jan-1981 #sequence revision 18-Aug-1982 #text_change 09-Jul-2004 A 934343 536861, 533887, 990563; A90564; B91668; A91723; A02146	Nucleic Acids Res. 10, 4071-4079, 1982 A; Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A; Reference number: A93433; MUD:8224238; PMID:6287432 A; Accession: A93433 A; Molecule type: DNA A; Residues: 1-330 <elld a;="" coss-references:="" cross-references:="" embl:217370="" embl:217370<="" td="" uniprot:p01857;=""><td>1330 is removed after translation L.J. C. the EMBL Data Library, October 1992 a number: S33904 1; S3661 type: DMA 2. 2-330 «HAR»</td><td>ferences: EMBL:217370 1. N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T. 11-679, 1982 tructure of human immunoglobulin gamma genes: implications for evol</td><td>n untber: S338B7; MUID:83001943; PMID:6811139 n: S338B7 type: DNA 88-1113:235-330 <tak>:</tak></td><td>1.J.</td><td>a number: A90563; MOLD:/L064024; PMLD:5489771 : myeloma protein Bu n: B90563 type: protein</td><td>: 1-96,'R', 98-135 <cun> ss equence has the GIM(3) marker, 97-Arg ss requence has the GIM(3) marker, 97-Arg ss Y, 3121-3181, 1970 ry 9, 3171-3181, 1970 ry 9, 3171-3181, 1970 e rovalent structure of a human gammaG-immunoglobulin. VIII. Amino e number: A90564; MUID:71064025; PMID:5530842 Eu</cun></td><td>ccession: A90564 Glecule type: protein status: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-2</td></elld>	1330 is removed after translation L.J. C. the EMBL Data Library, October 1992 a number: S33904 1; S3661 type: DMA 2. 2-330 «HAR»	ferences: EMBL:217370 1. N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T. 11-679, 1982 tructure of human immunoglobulin gamma genes: implications for evol	n untber: S338B7; MUID:83001943; PMID:6811139 n: S338B7 type: DNA 88-1113:235-330 <tak>:</tak>	1.J.	a number: A90563; MOLD:/L064024; PMLD:5489771 : myeloma protein Bu n: B90563 type: protein	: 1-96,'R', 98-135 <cun> ss equence has the GIM(3) marker, 97-Arg ss requence has the GIM(3) marker, 97-Arg ss Y, 3121-3181, 1970 ry 9, 3171-3181, 1970 ry 9, 3171-3181, 1970 e rovalent structure of a human gammaG-immunoglobulin. VIII. Amino e number: A90564; MUID:71064025; PMID:5530842 Eu</cun>	ccession: A90564 Glecule type: protein status: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-2

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F;20-84/Domain: immunoglobulin homology <IMM>
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Best Local Simi:
Matches 110; (
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Daccession: PS0019; Begquence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: PS0019; D25941
R;Brueggemann, M.
Gene 74, 473-482, 1988
A;Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.
A;Reference number: PS0017; MJID:89232738; PMID:3149946
A;Reference number: PS0017; MJID:89232738; PMID:3149946
A;Residues: 1-322 < BRUS
A;Residues: 1-322 < BRUS
A;Residues: 1-322 < BRUS
A;Reference number: A25941; MJID:86287397; PMID:3016742
A;Reference number: A25941; MJID:86287397; PMID:3016742
A;Reference number: A25941; MJID:86287397; PMID:3016742
A;Residues: 216-222 < BRZ>
C;Genetics:
A;Introns: 98/1; 109/1; 216/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: immunoglobulin
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C;Species: Sus scrofa domestica (domestic pig)
C;Accession: 147162
R;Accession: 147162
R;Kacskovics, 1.; Sun, 3.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequence A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequence A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Reference number: 1277 < KAC>
A;Residues: 1-277 < KAC>
A;Geneules: 1-277 < KAC>

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24.1%; Score 447; DB 2; Length 27
Best Local Similarity 34.3%; Pred. No. 4.8e-26;
Matches 97; Conservative 57; Mismatches 109; Indels
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Spannar until Claylor latural (domestic rabbit)
C;Species: Oryccolagus craitolius (domestic rabbit)
C;Species: Oryccolagus craitolius (domestic rabbit)
C;Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #text change 09-Jul-2004
C;Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #text change 09-Jul-2004
C;Date: 12-4-Apr-1984 #sequence revision 15-Nov-1984 #text change 09-Jul-2004
R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A;Title: Rib Reguence of a rabbit IgG heavy chain from the recombinant F-I haplo
A;Accession: A91749
A;Accession: A91749
A;Accession: A91749
A;Accession: Bis sequence studies on the constant region of the Fd sections of rabbit immunoglo
A;Accession: A90290
A;Acces
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A; Residues: 88-103, M', 105-143, E', 145-184, A', 186, 'E', 188-266 < MAR>
A; Cross-references: Gs.M16426; NID:g165111; PIDN:AAA31289.1; PID:g165112
A; Note: this sequence has the dil allotypic marker, 104-Met, and the e15 allotypic mark
R; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
B; Fruchter, R.G.; Sequence studies of the Fd section of the heavy, chain of rabbit immunoglobulin
A; Title: Sequence studies of the Fd section of the heavy, chain of rabbit immunoglobulin
A; Reference number: A90245; MUID:70110015; PMID:5461106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wiksell
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A;Residues: 132-143,'E',145-161 <FRU>
FHILL, E.D., LEDOVILE, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and
A;Reference number: A94416
                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSSTW-SSQAVTCNVAHPASSTKVDKKIVPREC---NPCGCTGSEVSSVFIFPPKTKDVL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202
                                                                                                                                                                                                                                                                                                                                                                                                                                         94 TQGQWMSSNTYTCHVKHNGSIFEDSS----RKCADSNPRGV-----SAYLSRPSFFD-L 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVY-MLPPSPEETGTTRTVTCLIRG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYPSEISVOWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYGRMLVNKSIWEKGNLVTCRV 321
                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                      19 SNSMVTLGCLVKGYFPEPVTVTWNSGALSSG----VHTFPAVLQ-----SGLYTLTSSVTV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 FYPPDIYTEWKANGQPQE--NYKNTPPTMD--TDGSYFLYSKLNVKKETWQQGNTFTCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIRKSPIITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 AHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNI
                                                                                                             33;
Length 322;
                                                                                                                   Indels
23.9%; Score 443.5; DB 2; 34.4%; Pred. No. 1.1e-25; live 50; Mismatches 127;
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A;Cross-references: UNIPROT:P20762; EMBL:X07189; NID:957602; PIDN:CAA30169.1; PID:966322
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-84/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Dec.1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
Ciscession: S00847
Ribrueggemann, M.; Delmastro-Galfre, P.; Waldmann, H.; Calabi, F.
Bur. J. Immunol. 18, 317-319, 1988
A;Title: Sequence of a rat immunoglobulin gamma-2c heavy chain constant region cDNA: A;Reference number: S00847; MUID:88166903; PMID:3127222
A;Accession: S00847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSPEETGTTR-TVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 PPREQMSKNKVSLTCMVTSFYPASISVEWERNGELEQ--DYKNTLPVLD--SDESYFLYS 290
                                                                                                    141
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                                                                                                                                                                                                                                                                                                                                                                                                                         320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 REGGQIFSLQSEVNITQGQMMSSNTYTCHVKH----NGSIFEDSSRK-----CA-D 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---SGLYTLSSSVTVPSSTW-SSQTVTCSVAHPATKSNLIKRIEPRRPKPRPFTDICSCD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 SNPRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 DNLGRPSVFIFPPKREKDIMITLTPKVTCVVVDVSEBEPDVQFSWFVDNVRVFTAQTQPH 174
93
                                               70
                                                                                                                                                                                                                                              LIILLIPKVTCVVVDISQDDPEVHFSWFVDDVEVHTAQTRPPEEQFNSTFRSVSELPILH
                                                                                                    -- DSSRKCADSNPRGVSAYLSRPSPFD-
                                                                                                                                         71 PSSTW-PSQTVTCNVAHPASSTKVDKKIVPRNCGGDCKPCICTGSEVSSVFIFPPFKFKDV
                                                                                                                                                                                                         LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                                                                                                                                                                                 202 RDWIEGETYQCRVTHPHLPRALMRSTIKLPGKRLAPEVYMLPPSPEE-TGTTRTVTCLIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 PTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLP
                                               19 SNSMVTLGCLVKGYFPEPVTVTWNSGALSSG----VHTFPAVLQ-----SGLYTLTSSVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 psvyplvpgcs--drsgslvtlgclvkgyfpepvrvkwnsgalssg---vhtfpavlQ--
AHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLPPYTTRPKREGGQTFSLQSEVNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

23.1%; Score 428; DB 2;
Best Local Similarity 32.4%; Pred. No. 1.5e-24;
Matches 110; Conservative 59; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 VVHEALPGSRTLEKSLHYSAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 VLHEGLHNHHT-EKSLSHSPG 325
                                                                                                       94 TQGQWMSSNTYTCHVKHNGSIFE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
     38
                                                                                                                                                                                                                                                                 130
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Ig gamma-1 chain C region - rat

() Species: Rattus norvegicus (Norway rat)

C) Species: Rattus norvegicus (Norway rat)

C) Species: Rattus norvegicus (Norway rat)

C) Accession: DS0017; C25941

R) Brueggemann, M.

Gare 74, 473-482, 1988

A,Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.

A,Reference number: PS0017; MUID:89232738; PMID:3149946

A,Reference number: PS0017

A,Molecule type: DNA

A,Residues: 1-326 ABNA

A,Reference number: Residues: Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.

Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986

A,Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibod

A,Reference number: A25941; MUID:86287397; PMID:3016742
  A; Molecule type: protein
A; Residues: 129-131; 155-172, 'D', 174-184,'A', 186,'E', 188-200,'D', 202-217,'E', 219-232,'Q',
A; Residues: 129-131; 155-172,'D', 174-184,'A', 186,'E', 188-200,'D', 202-217,'E', 219-232,'Q',
A; Note: this has the e15 allotypic marker, 185-Ala
C; Complex: An immunoglobulin hererotetramer subunit consists of two identical light (kap; hain disulfide bonds. In some cases, such as 1gA and 1gM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin hemotogramer; immunoglobulin hemotogy *IM1>
F; 20-82, Domain: immunoglobulin homology *IM2>
F; 236-303, Domain: immunoglobulin homology *IM3>
F; 236-303, Domain: immunoglobulin homology *IM3>
F; 173, Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10,
                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNITOGOWMSSNTYTCHVKH-----NGSIFEDSSRKCADSNPR---GVSAYLSRPSPF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 DILMISRIPEVICVVVDVSQDDPEVQFIWYINNEQVRIARPPL-----REQÓFNSTIRV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 VSTLPITHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTWGPPREELSSRS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D-LFIRKSPTITCLVVDLAPSKGTVNLTW-----SRASGKPVNHSTRKEEKQRNGTLTV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 TSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVY-MLPPSPEETGTT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 RIVICLIRGEYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKSIWE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 GDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRT---FPSV----RQSSGLYSLSSV 68
                                                                                                                                                                                                                                                                                                                                                                                                                              36 GDA-HSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPKREGGQTFSLQSE
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                                                                                                                                                                                                                                                                                                                    Query Match 23.6%; Score 437.5; DB 1; Length 323; Best Local Similarity 34.3%; Pred. No. 2.9e-25; Matches 113; Conservative 61; Mismatches 110; Indels 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 326;
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A;Molecule type: DNA
A;Residues: 220-326 <BR2>
C;Genetics:
A;Introns: 98/1; 113/1; 220/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-84/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGDVFTCSVMHEALHNHYT-QKSISRSPG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 KGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
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A.N.Creasing. 72.20

A.R.Creasing. 72.20

A.R.Creasing. 72.20

A.R.Creasing. 72.20

A.R.Creasing. 118-267, E', 269-328, 'G', 330-334 <DOG>
C.Comment: Lys-335 is removed posttranslationally.
C.Complex: An immunoglobulin heterotetramer submit consists of two identical light (ka hain disulfide bonds. In some cases, such as 1gA and 1gM, the submits associate into 1 C.Superfamily: immunoglobulin C region; immunoglobulin homology
C.Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob F;08-118/Region: hinge
F;142-211/Domain: immunoglobulin homology <IM2>
F;248-315/Domain: immunoglobulin homology <IM3>
F;248-315/Domain: immunoglobulin homology <IM3>
F;248-315/Domain: immunoglobulin homology <IM3>
F;248-315/Domain: immunoglobulin (to light chain) #status predicted
F;15/Disulfide bonds: interchain (to heavy chain) #status predicted
F;108,117/Disulfide bonds: interchain (to heavy chain) #status predicted
F;185/Binding site: carbobydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iggamma-2a chain C region, secreted form (allele b) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A02153; A32656
R;Schreier, P.H.; Bothwell, A.L.M.; Mueller-Hill, B.; Baltimore, D.
Proc. Natl. Acad. Sci. U.S.A. 78, 4455-4499, 1981
A;Title: Multiple differences between the nucleic acid sequences of the IgG2a(a) and A;Title: Multiple differences between the nucleic acid sequences of the IgG2a(a) and A;Title: Multiple differences between the nucleic acid sequences of the IgG2a(a) A;Reference number: A02153
A;Cossion: A02153
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108 PKCPPPENLGGPSVFIFPPEKEKDTLMISLIFPRVICVVVDVSQDEPEVQPTWF-VDNKPVG 166
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                                                                                                                                                                                                                                                                                                                                                                                               227 PDVYTLPPSRDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKNTPPIED--AD 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQ 186
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                                                                                                                                    NHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLA
                                                                                                                                                                                                                         167 NAETKPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRM
                                                                                                                                                                                                                                                                                                              PEVYML PPSPEETGTTR - TVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTTRPQKDHGTD
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Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981
Afritle: Multapple amino acid substitutions between murine gamma A; Reference number: A32656; MUID:82037777; PMID:6794027
A; Accession: A32656
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Best Local Simi
Matches 106;
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A;Residues: 227-311 A70.28

R;Oliveira, B; Lamm, M.E.

B;Ochemistry 10, 26-31, 1971

A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.

A;Title: Interchain disulfide bonds

A;Title: Interchain disulfide bonds

A;Tontents: annotation; disulfide bonds

A;Contents: annotation; disulfide bonds

A;Note: Cys-16; Is involved in a heavy-light chain bond

A;Note: Cys-16; Cys-107, and Cys-110 form inter-heavy chain bonds

A;Note: Cys-16; Cys-107, and Cys-110 form inter-heavy chain bonds

C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin homology <IM1>
F;21-81/Domain: immunoglobulin homology <IM2>
F;24-310/Domain: immunoglobulin homology <IM3>
F;24-310/Domain: immunoglobulin homology <IM3>
F;24-310/Domain: immunoglobulin homology <IM3>
F;24-310/Domain: immunoglobulin homology <IM3>
F;24-310/Domain: immunoglobulin experimental
F;178/Binding site: carbohydrate (Asn) (covalent)
F;248-308/Disulfide bonds: #status experimental
F;248-308/Disulfide bonds: #status experimental
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A; Molecule type: protein
B; M; Rsiduces: 69-133;312-329 < TUR>
B; Tracey, D. B.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
B; Chemistry 13, 4796-4803, 1974
A; Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A; Reference number: A90384; MUID: 75036072; PMID: 4429665
A; Accession: A90384
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Residues: 134-226 <TRA>
Trischmann, T.M.; CEDra, J.J.
icchemistry 13, 4804-4811, 1974
Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A;Residues: 1-3 cTRI>
A;Cross-references: UNIPROT: P01862
B;Cross-references: UNIPROT: P01862
B;Chemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III.
A;Reference number: A90352; MUID:71058471; PMID:5538606
A;Accession: A90352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: protein A, Residues: 4-68 < BIR> A, Residues: 4-68 < BIR> B. Carry, 1.0. Gebra, K.J.; Cebra, K.J.; Cebra, K.J.; Cebra, K.J.; Cebra, K.J.; Cebra, K.J.; Cebra, K.J.; L.J. 1971
Blochemistry 10, 9-17, 1971
A, Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. A, Reference number: A90359; MUID:71058486; PMID:5538616
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                  Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: O7-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
C;Date: O7-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
C;Accession: A94553, A90352; A90384; A90385; A02151
R;Trischmann, T.M.
submitted to the Atlas, April 1975
A;Reference number: A94553
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RESULT 15
(20554
19 heavy chain C region - sheep (fragment)
(;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
(;Species: Ovis orientalis aries, Covis ammon aries (domestic sheep)
(;Species: Ovis orientalis aries, Covis ammon aries (domestic sheep)
(;Date: Oliver, 2015)
(;Accession: C30554
(;Imunol: 142, 708-711, 198)
(;Arile: Isolation and sequence of sheep Ig H and L chain cDNA.
(A,Reference number: A30554; MUID:89093962; PMID:2492052
(A,Status: preliminary; not compared with conceptual translation
(A,Molecule type: mRNA
(A,Residus: 1-308 *FOLA)
(C,Superfamily: immunoglobulin C region; immunoglobulin homology
(C,Keywords: heterotetramer; immunoglobulin homology < (C,Keywords: heterotetramer; immunoglobulin < (C,Keywords: h
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144
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22.5%; Score 418; DB 2; Length 308;
Best Local Similarity 33.3%; Pred. No. 7.9e-24;
Matches 106; Conservative 54; Mismatches 122; Indels 36;
                                                                                                                                                                                                                     300 VOKSTWERGSLFACSVVHEVLHNHLTTKTISRSL 333
                                                                                                                                                                   306 VNKSIWEKGNLVTCRVVHEALPG---SRTLEKSL 336
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P01859 homo sapien
Q95m34 equus cabal
P01861 homo sapien
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Bac8234 homo sapi
Géptis homo sapien
Gégmxy homo sapien
Aah2944 homo sapien
Q90524 ginglymosto
Oépih7 homo sapien
                                                                                                                                                                         November 14, 2004, 15:03:40 ; Search time 97 Seconds (without alignments) 2028.641 Million cell updates/sec
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1 EFHHHHHTLSLPESGPVTI......HEALPGSRTLEKSLHYSAGN 342
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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090545 ginglymosto	090529 ginglymosto			Ofgmx0 homo sapien	Q6p491 homo sapien	Aah63599 homo sapi	Q6qmw1 homo sapien	090530 ginglymosto	07z473 homo sapien	Bac85358 homo sapi	Q6qmw3 homo sapien	P20763 gallus gall	
090545	090529	Q7Z3Y4	Q6GMX8	Q6GMX0	Q6P491	AAH63599	Q6GMW1	090530	072473	BAC85358	Q6GMW3	LAC CHICK	BAC85236
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166.5	165.5	165	16,	16	162.5	162		16	• •	15	•	• •	_

ALIGNMENTS

90 **8**9

29; Gaps

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259 IRGEYPSEISVOWLENNEEDHTCHHTTTRPQKDHGTDPSFFLYSRMLVNKSIWEKGNLVT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 VKGFYPSDIAVEWESNGQPEN--NYKTTPPMLD--SDGSFFLYSKLTVDKSKWQQCNVFS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98383416; PubMed-9717671; Wagner B., Overesch G., Sheoran A., Holmes M., Richards C., Leibold W., Radbruch A.; Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."; Immunobiology 199:105-118(1998).
                                                                                                                                                                                                                                                69 VIVPSSNF-GIQIYICNVDHKPSNIKVDKIVERKCCVECPPCPAPPVAGPSVFLFPPKPK
                                                                                          35 RGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPKREGGQTFSLQSE
                                                                                                                                        16 RSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG---VHTFPAVL----QSSGLYSLSSV
                                                                                                                                                                                                91 VNITOGOWMSSNIYTCHVKH---NGSIFEDSSRKCADSNP-----RGVSAYLSRPSPF
                                                                                                                                                                                                                                                                                                         D-LPIRKSPITICLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEBKQRNGTLTVTSTLPV
                                                                                                                                                                                                                                                                                                                                        200 GIRDWIEGETYQCRVTHPHLPRALMRSTIKLPGKRLAPEVYMLPPSPEE-TGTTRTVTCL
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X MEDLINE=22172648; PubMed=12185539;

A Wagner B., Greiser-Wilke I., Wege A.K., Radbruch A., Leibold W.;

IM Wagner B., Greiser-Wilke I., Wege A.K., Radbruch A., Leibold W.;

IM "Evolution of the six horse IGHG genes and corresponding in "town of the six horse IGHG genes and corresponding in munoglobulin gamma heavy chains.";

IM "Munogenetics 54:353-364(2002).

RE MELL, AJ30675; CAC44624.1;

DR HSSP; PO1857; 114e.

DR InterPro; IPR003100; Ig-like.

DR InterPro; IPR003597; Ig-c1.

DR InterPro; IPR00366; Ig-MHC.
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 29, Last sequence update)
01-DRAR-2004 (TrEMBLrel. 26, Last annotation update)
Immunogobulin gamma 1 heavy chain constant region (Fragment)
                 Pred. No. 2.4e-29;
'; Mismatches 120; Indels
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A60BF2B01DEFD1F6 CRC64;
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SMART; SMO0407; IG-1, 2.
PROSITE; PS0835; IG-IKE; 3.
PROSITE; PS00290; IG-MHC; UNKNOWN_2.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
36.2%; Pic.
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                                             117; Conservative
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01-DEC-2001 (
01-DEC-2001 (
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S -> A (in myeloma proteins TIL and ZIE)
FyrId-VAR 003899.

C -> S (in Ref. 3).
8310878C6878CF9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Milstein C., Frangione B.; "Disulphide bridges of the heavy chain of human immunoglobulin G2."; Biochem. J. 121:217-225(1971).
                                                                                                                                                                                                                                                                 SEQUENCE OF 1-121 (DOT).
MEDLINE-95255298; PubMed=7737190;
Stoppinim M., Bellotti V., Negri A., Merlini G., Garver F., Ferri "Characterization of the two unique human anti-flavin monoclonal immunoglobulins.";
                               Hofmann T., Parr D.M.; "A note of tesidues 381-391 of human
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GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0003823; P:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 3.
SWART; SMOMO,; IGLI; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
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Frangione B., Milstein C., Pink J.R.L.;
"Structural studies of immunoglobulin G.";
Nature 221:145-148(1969).
                                                                                                                                                      REVISIONS TO 25, 59, 60 AND 264-268 (ZIE) Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank.
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                                                   "A note of the amino actu sequentimentally sequentially sequent that it is a sequent to the sequent to the sequent to the sequent is sequent to the sequent 
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12;

Gaps

45;

Matches 113; Conservative

DB 1; Length 326;

Score 486.5;

26.2%;

Query Match

us-09-401-636-8.closed.rup

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                                                                                                                                                                   79 REGGOTFSLOSEVNITQGQWMSSNIYICHVKHNGSIFE------DSSRKCADSN--P 127
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                                                                        - SSGFYSLSSMVTVPASTW-TSETYICNVVHAASNPKVDKRIEPIPDNHQKVCDMSKCP
                                                                                                                                                                                                    VYMLPPSPEETGTTR-TVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPS
                                                                                                                                                                                                                  PTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPK
                               PKVFALAPGCGTTSD--STVALGCLVSGYFPEPVKVSWNSGSLTSG---VHTPPSVL---
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MEDLINE=70207560; PubMed=419269;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-83157104, PubMed-6299662,
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
                                                                                                                                                                                                                                                   FFLYSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
                                                                                                                                                                                                                                                                 YPLYSKLSVDRNRWQQGTTFTCGVMHEALHN-----HYTQKN 330
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21-JUL-1986 (Rel. 01, Last sequence update)
10-COT-2004 (Rel. 45, Last annotation update)
1g gamma-4 chain C region.
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MIM; 147130; -.

GO; GO:0005624; C:membrane fraction; NAS.

GO; GO:0003823; F:amtigen binding; TAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPR007110; Ig-11ke.

InterPro; IPR003597; Ig_C1.

InterPro; IPR003066; Ig_MHC.

Pfam; PF00047; ig; 3.
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PDB; LADQ; X-ray; A=118-323.
Genew; HGNC:5528; IGHG4.
MIM; 147130;
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P01861;
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MEDLINE-71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VII. Amino
acid sequence of heavy-chain cyanogen bromide fragments HI-H4.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
SMART; SM00407; IGC1; 2.
PROSITE; PSSOB35; IG LIKE; 3.
PROSITE; PSSOB309; IG LIKE; 3.
3D-structure; Direct protein sequencing; Immunoglobulin C region;
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35.8%; Pred. No. 1.5e-28;
ive 57; Mismatches 121; Indels
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21-UTL-1986 (Rel. 01, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Iggamma-1 chain C region.
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Ellison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human in
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327 AA;
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N-linked (GlcNAc. .).
K -> R (in GlM(3) marker).
/FIId=VAR.03886.
D -> E (in GlM(non-1) marker).
/FIId=VAR_003887.
L -> M (in GlM(non-1) marker).
/FIId=VAR_003888.
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Interchain (with heavy chain).
Interchain (with heavy chain).
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PDB; 1D6V; X-ray; H=1-101.
PDB; 1DAZ; X-ray; A/B=120-326.
PDB; 1E4K; X-ray; A/B=120-329.
PDB; 1E7L; X-ray; A/B=106-329.
PDB; 1FCZ; X-ray; A=110-329.
PDB; 1FCZ; X-ray; A=11-326.
PDB; 1HZH; X-ray; B/D=1-103.
PDB; 117Z; X-ray; B/D=1-103.
PDB; 117Z; X-ray; A/B=107-330.
PDB; 11XZ; X-ray; A/B=107-330.
PDB; 11XZ; X-ray; A/B=107-330.
PDB; 11XZ; X-ray; A/B=110-330.
PDB; 10QX; X-ray; A/B=119-330.
PDB; 2RCS; X-ray; A/B=119-330.
PDB; 2RCS; X-ray; H=1-103.
Genew; HGNC:5525; IGHG1.
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X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).

RA Deisenhofer J.;

Deisenhofer J.;

Crystallographic refinement and atomic models of a human Fc fragment are its complex with fragment B of protein A from Staphylococcus

The and its complex with fragment B of protein A from Staphylococcus

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                                                                                                                                                                                                                   SEQUENCE (MYELOMA PROTEIN NIE).

MEDLINE=77070269; PubMed=826475;

Ponstingl H., Hilschmann N.;

"The rule of antibody structure. The primary structure of a monoclonal iggl immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
                                                                                                                                      Amino
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
MEDLINE=83289131, PubMed=6884994,
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
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Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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MEDLINE=71064027; PubMed=4923144;
Gall W.E., Bdelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
                                                                                 Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H., Edelman G.M.,
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PIR; A9433; GHHU.
PDB; IAJ7, X-ray; H=1-103.
PDB; IDSB; X-ray; B/H=1-101.
PDB; IDSI; X-ray; H=1-101.
                             [3]
SEQUENCE OF 136-329 (EU).
MEDLINE=71064025; PubMed=5530842;
      Biochemistry 9:3161-3170(1970).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 TQGQWMSSNTYTCHVKHNGSIFEDSS----RKCADSNPRGV-----SAYLSRPSPFD-L 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 AHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNI
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Ovyctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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05-JUL-2004 (Rel. 44, Last annotation update)
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use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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10; Conservative
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SEQUENCE FROM N.A.
BEDLINE=89232738; PubMed=3149946;
Brueggemann M.;
"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 74:473-482(1988).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                        Bernstein K.E., Alexander C.B., Mage R.G.; "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                                                                                              region of the Fd sections of rabbit
                                                                                                                                                                                                                               MEDLINE-83299917; PubMed-6193512;
MEDLINE-83299917; PubMed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit 1gG: isolation of a cDNA encoding gamma heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "INSCELLANEOUS: Ref.1 sequence has the D12 allotypic marker, 104-
Thr, and the E14 marker, 185-Thr. Ref.3 has the D11 and E15
markers and Ref.5 the E15 marker.
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                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=70110015; PubMed=5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.,
"Sequence studies of the Fd section of the heavy chain of rabbit
imminod.obulin G.";
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T -> A (IN B15 MARKER).
V -> V (IN B15 MARKER).
V -> E (IN REf. 2).
Q -> E (IN Ref. 3 and 4).
N -> D (IN Ref. 5).
Q -> E (IN Ref. 5).
E -> Q (IN Ref. 5).
E -> G (IN Ref. 5).
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Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, M16426; AAA31289.1; -.
PIR, A91749; GHRB.
HSSP, PO1852; INFD.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfan, PF00047; Ig.3.
SMART; SM00407; IGc1; 2.
PROSTIE; PS50815; IG_LIKE; 3.
PROSTIE; PS00290; IG_HHC; 1.
Direct protein sequencing; Immunoglobulin C region; Immunoglobulin domain; Repeat.
                                                                                       SEQUENCE OF 1-128.
MEDLINE=76135465; PubMed=1243651;
Pratt D.M., Mole L.E.; Requence studies on the constant region cimmunoglobulin G of different allotype.";
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Ig-like 3.
       MEDLINE=84030930; PubMed=6313520;
                                                         f-I haplotype.";
Immunogenetics 18:387-397(1983)
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                                                                                                                                                                                                                                                                                                                                      36 GDA-HSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPKREGGQTFSLQSE
                                                                                                                                                                                                                                                                                                                                                                                                           16 GDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRT---FPSV----RQSSGLYSLSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 VNITOGOWMSSNIYICHVKH-----NGSIFEDSSRKCADSNPR---GVSAYLSRPSPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 D-LFIRKSPTITCLVVDLAPSKGTVNLTW-----SRASGKPVNHSTRKEEKQRNGTLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 ISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVY-MLPPSPEETGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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Brueggemann M.;
"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
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N -> D (in Ref. 5).

N -> D (in Ref. 5).

Y -> W (in Ref. 5).

N -> S (in Ref. 5).

N -> S (in Ref. 5).
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                                                                                                                                                                                                                                            ; Pred. No. 1.4e-25; 61; Mismatches 110;
                                                                                                                                                                                                       Score 437.5; DB
Pred. No. 1.4e-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 KGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
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RGDVFTCSVMHEALHNHYT-QKSISRSPG 322
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CH2.
CH3.
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al Similarity 34.3%;
113; Conservative 6:
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329 AA;
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hes 110;
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LTITLTPKVTCVVVDISQDDPEVHFSWFVDDVEVHTAQTRPPEEQFNSTFRSVSELPILH 189
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                                                                                                                                                                                                        38 AHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNI 93
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MEDIJNE=88166903; PubMed=3127222;
MEDIJNE=88166903; PubMed=3127222;
Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
                                                                                                                                                                                                                                           SNSWVILGCLVKGYFPEPVTVIWNSGALSSG----SGLYTLISSSVTV
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Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                         94 TQGQMMSSNTYTCHVKHNGSIFE------DSSRKCADSNPRGVSAYLSRPSPFD-
                                                                                                                                                                                                                                                                                                                                                                                  71 PSSTW-PSQTVTCNVAHPASSTKVDKKIVPRNCGGDCKPCICTGSEVSSVFIFPPKPKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                             LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
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                                                                                                                                                   Gaps
   .) (Potential).
                                                                                                                                                   31;
                                                                                       Length 326;
                                                                                                                                                   Indels
N-linked (GlcNAc. . .) (Post of the control of the 
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R4SSP; P01864; LBOG

R InterPro; IPR001309; Ig-like.

R InterPro; IPR003006; Ig-MHC.

Pfam; PF00047; Ig; 2.

SMARY: SMO0407; IgG-1; 2.

SMARY: SMO0407; IGG-1; 2.

PROSITE; PS00290; IG_MHC; 1.

Imunoglobulin C region; Immunoglobulin domain.

DOMÄIN 1 97 CH1
                                                                                 23.5%; Score 436.5; DB 1; 32.7%; Pred. No. 1.7e-25; ive 54; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
19 gamma-2C chain C_region.
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                               35946 MW;
                                                                                                                                                Conservative
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                            326 AA;
                                                                                                                    Best Local Similarity
Matches 105; Conser
CARBOHYD
SEQUENCE
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P20762;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 SNPRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNLGRPSVFIFPPKPKDILMITLTPKVTCVVVDVSEEEPDVQFSWFVDNVRVFTAQTQPH 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                6 PSVYPLVPGCS --GTSGSLVTLGCLVKGYFPEPVTVKWNSGALSSG---VHTFPAVLQ--
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MEDLINE-71056486; PubMed=5538616;
Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea pig immunoglobulin-
(2). II. Amino acid sequence of the carboxyl-terminal and hinge
region cyanogen brominde fragments.";
Biochemistry 10:9-17(1971).
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Birshtein B.K., Hussain Q.Z., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea pig immunoglobulin-
"G(2). 3. Amino acid sequence of the region around the half-cystine
joining heavy and light chains.";
Biochemistry 10:18-25(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOTO CAVPO STANDARD; PRT; 329 AA.

P01862;
P01862;
P01862;
P01862;
P01-1986 (Rel. 01, Last sequence update)
P05-JUL-1986 (Rel. 44, Last annotation update)
D1-JUL-1986 (Rel. 44, Last annotation update)
D2-JUL-2004 (Rel. 44, Last annotation update)
D3-JUL-2004 (Rel. 60)
D4. As annotation update)
D5-JUL-2004 (Guinea pig).
Cavia porcellus (Guinea pig).
Cavia porcellus (Guinea pig).
Mammalia; Butheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                              (with a light chain)
                                                                                                                              chain)
                                                                                                                                                                                                                                                                                         Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 REGGQTFSLQSEVNITQGQWMSSNTYTCHVKH----NGSIFEDSSRK-
                                                                                                                              (with a heavy (with a heavy
                                                                                                                                                                                                                                         36571 MW; SFCD7B7933850773 CRC64;
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                                                                                                                                                                                                                                                                                                                   ; Pred. No. 7.8e-25; 59; Mismatches 134;
                                                                                                                                                                                                                                                                                            23.1%; Score 428; DB 1; 32.4%; Pred. No. 7.8e-25;
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Submitted (APR-1975) to the PIR data bank.
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                                                                                                                                    Interchain
                                                                                                                                                          Interchain
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GCAB MOUSE
P01864;
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                                                                                                                                                                                                                              Biochemistry 10:26-31(1971).
-!- MISCELLANEOUS: This chain was isolated from pooled serum of strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 LQ----SGLYSLTSMVTVP----SQKATCNVAHPASSTKVDKTVEPIRTPZPBPCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KC-ADSNPRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 NAETKPRVEQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRM
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                                                                                                                                                                                     MEDDINE-1058474;
MIDDINE-1058474;
Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19. TIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                          [5]
SEQUENCE OF 227-311.
MEDLINE=75036073; PubMed=4609467;
Trischmann T.M., Cebra J.J.;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2
SEQUENCE OF 134-226.
BIRDILNES-7036072. PubMed-4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
                                                                                                                                                                                                                                               13 inbred guinea pigs.

13 inbred guinea pigs.

PIR; A9455; G2GP.

INSSP: POR1842; 7FAB.

Interbro; IPR003101; Ig-like.

Interbro; IPR003106; Ig-MHC.

Fam; PF0047; ig; 2.

SMART; SM00407; ig; 2.

SMART; SM00407; ig; 2.

SMART; SM00209; IG-MHC.

PROSITE; PS00209; IG-MHC; 1.

Direct protein sequencing; Glycoprotein; Immunoglobulin C region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Interchain (with a heavy chain).
Interchain (with a heavy chain).
Interchain (with a heavy chain).
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, Pred. No. 1.4e-24;
52; Mismatches 136; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                       Interchain (with a light chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSFFLYSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36074 MW; 5D231B7164D1FBA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-linked (GlcNAc. . .).
                                                              Biochemistry 13:4796-4803(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.9%;
33.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 33.2 es 115; Conservative
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1107
1110
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79
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105
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142
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329 AA;
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RESULT 10

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                               Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.; "Multiple differences between the nucleic acid sequences of the IgG2aa and IgG2ab alleles of the mouse."; Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
                                                                                                                                                                                                                                                                                                                                            gamma 2a heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note=Probably the major isoform;
Name=Membrane-bound;
Name=Membrane-bound;
Isold=P01865-1; Sequence=External;
-!- MISCELLANEOUS: The sequence differs from that of the a allele, from BALB/c mice, at 15% of the positions.
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REMBL, J00479; -; NOT_ANNOTATED_CDS.

R PDB; 1BOG; X-ray; B=1-101.

R PDB; 1HH6; X-ray; B=1-101.

R PROSITE; PS002300; IG_MHC.

R PROSITE; PS002300; IG_MHC; 1.

R PROSITE; PS002200; IG_MHC; 1.

R PROSITE; Alternative splicing; Direct protein sequencing; Normannoglobulin Gomain; Repeat.
                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                            21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
21-UL-1986 (Rel. 45, Last annotation update)
19 gamma-2A chain C region secreted form (B allele).
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                             Dognin M.J., Lauwereys M., Strosberg A.D.,
"Multiple amino acid substitutions between murine
Fc regions of Igla and Iglb allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
335 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P01864-1; Sequence=Displayed;
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Ig-like 2.
Ig-like 3.
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MEDLINE=82037861; PubMed=6170065;
                                                                                                                                                                                                                                                                                               SEQUENCE.
MEDLINE=82037777; PubMed=6794027;
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                   NCBI_TaxID=10090;
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                                                                                                                                                                            GDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPXTTRPKREGGQTFSLQSEV 91
                                                                                                                                                                                               184 YNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALFSPIEKTISKPRGFVRAPQVYVLPPPA
                                                                                                                                                                                                                                                                                                -GVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQ
                                                                                                                                                                                                                                                                                                                                                         187 RNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSP
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MEDLINE=80012837; PubMed=113776;
ROGETS J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-80202559; PubMed=6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seldman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=80045036; PubMed=115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mamo Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                     50;
                                                                                                                     Length 335;
                                                                                                                                                                                                                                      92 NITOGOWMSSNIYTCHVKHNGSIFEDSSRKCADSNPR-------
                                                                                                                                                 Indels
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                                                                                         36596 MW; FA3382792CBB13C6 CRC64;
                                                                                                                  Query Match
22.7%; Score 421; DB 1; L/Best Local Similarity 31.7%; Pred. No. 2.7e-24;
Matches 106; Conservative 54; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNKSIWEKGNLVTCRVVHEALPG---SRTLEKSL 336
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
gamma-1 chain C region secreted form.
Mus musculus (Mouse)
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Nucleic Acids Res. 6:3305-3321(1979)
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335 AA;
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P01868;
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                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     And State St
SEQUENCE (MYELOWA PROTEIN MOPC 21).
MEDLINE=78242288; PubMed=98524;
Adetugbo K.;
"Evolution of immunoglobulin subclasses. Primary structure of a murine
                                                                                                                                         DISTURIDE BONDS (MOPC 21).

MEDILINE=73008889; PubMed=5073237;

Svasti J., Milstein Ges.

"The distulphide bridges of a mouse immunoglobulin G1 protein.";

Biochem. J. 126:837-850(1972).

-I - SUBCELIULIAR LOCATION: Secreted.

-I - ALTERNATIVE PRODUCTS:

EVENT.=ALTERNATIVE SPLICING; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           light chain).
heavy chain).
heavy chain).
heavy chain).
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N -> D (in Ref. 3).
A338812F3D1F2C93 CRC64;
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                                                                                                                                                                                                                                                                                                                                        IsoId=P01868-1; Sequence=Displayed;
Note=May be the major isoform;
Name=Membrane-bound;
                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P01869-1; Sequence=External;
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Hinge.
CH2.
CH3.
                                                                                        myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978)
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EMBL; V00795; CAA24176.1; -.
PIR; A02159; GIMS.
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324 AA;
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REPEAT
12;
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                                                                                                                                                                        78 KREGGQIFSLQSEVNITQGQWMSSNIYICHVKHNGS-----IFEDSSRK-CADSNPR 128
                                                                                                                                                                                                                                                                                        188 NGTLIVISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPE 247
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MEDLINE=82247815; PubMed=6808505;
Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
Franklin E.C., Hood in disease in man: cDNA sequence supports partial gene
                                                                                                                                                                                                                                                                                                                                                                                    22 PPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRP
                                                                                                                         5 PPSV--YPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSG---VHTFPAVLQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-81021548; PubMed-6774747;
Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
Primary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  deletion model.";
Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264 (1982).
-!- SUBUNT: Dimer linked by 12 disulfide bonds; it has an extra interchain disulfide bond at position 7 in addition to the 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS TO 12-97 (PROTEIN WIS).
MEDLINE=77118561; PubMed=402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
Michaelsen T.E., Frangione B., Franklin E.C.;
Wrimary structure of the 'hinge' region of human IgG3. Probable quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIANE=77021516; PubMed=823945; Wolfenstein-Todel C., Franklin B.C.; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin B.C.; The amino acid sequence of 'heavy chain disease' protein ZUC. Structure of the Frankent of immunoglobulin G3."; Biochem. Biophys. Res. Commun. 71:907-914(1976).
    Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1g gamma-3 chain C region (Heavy chain disease protein) (HDC)
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC)
DB 1;
22.4%; Score 415.5; DB 1; 31.6%; Pred. No. 7e-24; ive 60; Mismatches 138;
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                                                 Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                         Best Local Similarity
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P01860;
       Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                               Disease protein WIS is lacking most of the V region
                                                                                          MISCELLANDEOUS: Disease protein WIS is lacking most of the V region and all of the CH1 region.

MISCELLANDEOUS: Disease protein ZUC lack most of the V region, all of the CH1 region, and part of the hinge compared with normal gamma-3 heavy chains.

MISCELLANDEOUS: Disease protein OWM may represent an allelic form or another gamma chain subclass.

MISCELLANDEOUS: The hinge region in gamma-3 chains is about four times as long as in other gamma chains and contains three identical 15-residue segments preceded by a similar 17-residue
normally present in the hinge region.
MISCELLANDOUS: The heavy chain disease protein WIS is shown.
MISCELLANDOUS: The sequence of residues 42-76 was taken from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain dimer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain dimer)
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Interchain (with heavy ch Interchain (with heavy
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/FTId=VAR 003890.
P -> L (in OMM).
/FTId=VAR 003891.
F -> Y (in OMM).
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T -> A (in OMM).
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/FTId=VAR 00389
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GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0003823; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003006; IG_NMC.
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HSSP; P01857; 1E4K.
Genew; HGNC:5527; IGHG3.
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                                                                                                                                                                                                                                           GVSAYLSRPSPFD-LPIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQR
                                                                                                                                                                                                               188 NGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ollo R., Rougeon F.;
"Mouse immunoglobulin allotypes: post-duplication divergence of gamma 22 and gamma 2b chain genes.";
Nature 296:761-763 (1982)
                                                                                     Gaps
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MEDLINE=80081501; PubMed=117548;

Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;

"Structure of the constant and 3' untranslated regions of the murine gamma 2b heavy chain messanger RNA.";
Science 206:1299-1303 (1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ALLELE A).

MEDLINE=80120716; PubMed=6766534;
Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
"Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from newborn nouse DNA.";
Nature 283:786-789(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94216359; PubMed=7512967; Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K., Irimura T., Takahashi N., Kato K., Arata Y.; "O-21/Yosoylation in hinge region of mouse immunoglobulin G2b."; J. Biol. Chem. 269:12345-12350(1994)
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R., "Sequence of the cloned gene for the constant region of murine gib immunoglobulin heavy chain."; science 206:1303-1306(1979).
                                                                                     7;
                                              Length 290;
                                                                                     Indels
E69CBC95705B2F46 CRC64;
                                         DB 1;
                                    Query Match 21.6%; Score 401.5; DB 1; Best Local Similarity 39.5%; Pred. No. 7.3e-23; Matches 85; Conservative 49; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                          341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-JUL-2004 (Rel. 44, Last annotation update)
19 gamma-28 chain C region secreted form
                                                                                                                                                                                                                                                                                                                                                                                                                   NKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG
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MEDLINE=80081502; PubMed=117549;
32331 MW;
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290 AA;
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GCB MOUSE
ID GCB MOUSE
AC P01866;
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IsoId=P01867-1; Sequence=External;
-!- PTM: O-linked glycan consists of Gal-GalNAc disaccharide which is modified with 2 stainc acid residues.
-!- MISCELLANBOUS: The a allele sequence is shown.
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
PINS, 255077, C2NS11.
InterPro; IPR007110; Ig-like.
InterPro; IPR00706; Ig-MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSGLYTMSSSVTVPSSTW-PSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 PPTVKLFHSSCDPRGD-AHSTIQLLCLVSGFSPAKVHVTWLVDGQEAENLFPYTTRPKRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPSVYPLAPGC---GDTTGSSVTLGCLVKGYFPESVTVTW-NSGSLSSSVH---TFPALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KCADSN-PRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNH
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                                                                                                                                                                                                                                 Pfam; PF00047; ig; 3. —
PROSTIE; PSS0835; IG_LIKE; 3.
PROSTIE; PS00290; IG_MHC; 1.
Alternative splicing; Glycoprotein; Immunoglobulin C region; Immunoglobulin domain; Repeat.
NON TER 1 1 1
DOMAIN 6 98 Ig-like 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).

By similarity.

By similarity.

O-linked (GalNAc. .).

Q -> R (in allele B).

N -> D (in allele B).

M -> I (in allele B).

L -> S (in Ref. 2 and 3).

S -> P (in Ref. 2 and 3).

I -> T (in Ref. 2 and 3).

M; 7D879662607C356E CRC64;
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Interchain (with
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IsoId=P01866-1; Sequence=Displayed;
Note=May be the major isoform;
Name=Membrane-bound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
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Interchain (1
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Ig-like 2.
Ig-like 3.
Interchain (
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336 AA;
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285 TYFLYSKLTVDTDSWLQGEIFTCSVVHEALHNHHT-QKNLSRSPG 328

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 TIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 S-TRKEEKORNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                         Ig gamma-3 chain C region, secreted form.

Mus musculus (Mouse).

Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

NCBI_TaxID=10090;
                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=85027161; PubMed=6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART, SM00407, 1g; 3.
SMART, SM00407, 1g; 3.
PROSITE; PS50835; IG_LKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Alternative splicing; Glycoprotein; Immunoglobulin C region; Immunoglobulin domain; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.4%; Score 397; DB 1; Length 329 Best Local Similarity 31.9%; Pred. No. 1.9e-22; Matches 110; Conservative 53; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 SFFLYSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
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                                                                                                  (Rel. 40, Last annotation update)
                                 329 AA
                                                                                 Last sequence update)
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CH2.
CH3.
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PIR; B02156; G3MSC.
                                                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig.MHC.
                                 STANDARD;
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114 2
224 3
329 AA;
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                               GC3 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-8122864; PubMed=6787604;
Ollo R., Auffray C., Morchamps C., Rougeon F.;
"Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic
                                                                                                                                                                                                                                                                                                                          MEDLINE-81198976; PubMed-6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene
and evolution of heavy chain genes: further evidence for intervening
                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-81076554; PubMed-6777755;
Sikorav J.-L., Auffray C., Rougeon F.;
"Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Implications
                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-OT-2004 (Rel. 45, Last annotation update)
Ig gamma-2A chain C region, A allele.
Mus musculus (Mouse).
Eukarolus (Mouse).
Mammalia; Butheria; Rodentia; Craniata; Wartebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDDINE=74175517; PubMed-4831970;
Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse 1gG2a
"immunoglobulin:amino-acid sequence of the Fc fragment. Implica
for the evolution of immunoglobulin structure and function.";
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330
                                                                                                                                                                                                                                                                                                                                                                                              sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981)
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PDB; 1E4W; X-ray; H=1-99.
PDB; 1E4X; X-ray; H/1=1-103.
PDB; 1MNU; X-ray; H=1-103.
InterPro; 1PR007110; Ig-like.
InterPro; 1PR00359; Ig_c1.
InterPro; PR003050; Ig_MHC.
Pfam; PF00047; ig; 2.
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STANDARD;
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                                                                                                                                                  NCBI_TaxID=10090;
GCAA MOUSE
            P01863;
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R PROSITE; SM00407; IGC1; 2.

R PROSITE; PS06295; IG_MHC; 1.

R PROSITE; PS06290; IG_MHC; 1.

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330 AA; 36389 MW; B84361C5445A6864 CRC64;
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SEQUENCE
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Sequence 6, 18 Sequence 6, 18 Sequence 6, 18 Sequence 4, 18 Sequence 4, 18 Sequence 4, 18 Sequence 6, 18 Sequen

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78 KREGGQIFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRKCADSNPRGVSAYLSRP 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08336583
Patent No. 5629415
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: HOLLIS, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN INVERSENCE ADDRESS:
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E.CARTY
STREET: 126 E. INNCOLN AVENUE
STREET: 126 E. INNCOLN AVENUE
STATE: NEW JERSEY
COUNTRY: RAHMAY
STATE: NEW JERSEY
COUNTRY: USA
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: DAW PC-DOS/MS-DOS
SOFTWARE: PATHIN PC-DOS/MS-DOS
SOFTWARE: PATHIN PC-DOS/MS-DOS
SOFTWARE: PATHIN PATA:
ATTONEY AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REPERRNCE/DOCKET NUMBER: 36,099
REPERRNCE/DOCKET NUMBER: 36,099
REPERRNCE/DOCKET NUMBER: 36,099
REPERRNCE/DOCKET NUMBER: 19211
TELEPOMMUNICATION INFORMATION:
TELEPAKX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.3%; Score 989; DB 1;
56.7%; Pred. No. 1.3e-87;
tive 53; Mismatches 84;
               US-08-024-253-6
US-08-477-460B-4
US-08-485-312A-4
US-08-485-312A-4
US-08-486-915-4
US-09-472-087-70
US-09-472-087-70
US-09-472-087-70
US-09-472-087-6
US-09-472-087-6
US-09-472-087-6
US-09-472-087-6
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US-09-472-087-6
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Matches 185; Conservative
single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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Best Local &
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                                                                                                                                                           November 14, 2004, 14:55:22; Search time 39 Seconds (without alignments) 581.558 Million cell updates/sec
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                                                                                                                                                                                                                                                          US-09-401-636-8
1856
1 BFHHHHHHHLSLPESGPVTI.......HEALPGSRTLEKSLHYSAGN 342
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-479-614-29
US-09-479-614-29
US-09-192-545-2
US-08-232-5399-56
US-08-802-096-1
US-09-802-096-1
US-09-802-096-1
US-09-802-096-1
US-09-802-096-1
US-09-802-998-1
US-09-808-998-1
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S-08-437-642B-23
S-08-146-206C-23
S-09-705-686-23
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Gaps

4;

Length 426;

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RESULT 3
US-09-479-614-14
US-09-479-614, Application US/09479614

Sequence 14, Application US/09479614

Sequence 14, Application US/09479614

Sequence 14, Application US/09479614

Sequence 10, 6573372

GENERAL INFORMATION: Feline Immunoglobulin E Molecules and Related Methods

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

FILE REFERENCE: P-1047

CURRENT FILING DATE: 2000-01-07

SERLIER FILING DATE: 1999-01-07

NUMBER: OF SEQ ID NOS: 34

SOFTWARE: PATENTIN VET: 2.0

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 14
256 TCLIRGFYPSEISVOWLFNNEEDHTGHHTTTRPOKDHGTDPSFFLYSRMLVNKSIWEKGN 315
                                                                                                                                                                    340 TCLIQNFFPADISVQWLRNDSPIQTDQYTTTGPHKVSGSRPAFFIFSRLEVSRVDWEQKN 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYM-LPPSPE-ETGTTRTV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 TCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKSIWEKGN 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 KREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRKCADSNPRGVSAYLSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 SPLDLYVHKSPKITCLVVDLANTDGMI-LIWSRENGESVHPDPMVKKTQYNGTITVTSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 VIIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQBAENLFPYTTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.4%; Score 972; DB 4; Length 431; 56:7%; Pred. No. 5.9e-86; ive 52; Mismatches 85; Indels
                                                                                                                                                                                                                                                         400 KFTCQVVHEALSGSRILQKWVSKTPG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 VFTCQVVHEALPGFRTLKKSVSKNPG 430
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US-09-479-614-2
US-09-479-614-2
Sequence 2, Application US/09479614
Patent No. 6573372
GENERAL INFORMATION:
APPLICANT: MCC211, Catherine
APPLICANT: Weber, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 56:7
Matches 185; Conservative
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ORGANISM: Felis catus
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                                                                                           280 PVNTNDWIEGETYYCRVTHPHLPKDIVRSIAKAPGKRAPPDVYLFLPPEEEQGTKDRVTL 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 KREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRKCADSNPRGVSAYLSRP 137
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                                                                                                                                                   PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPEETGTTR--TV 255
                                                                                                                                                                                                                               256 TCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKSIWEKGN 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESSE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13795
                                                                                                                                                                                                                                                                                                                                       400 KFTCQVVHEALSGSRILQKWVSKTPG 425
                                                                                                                                                                                                                                                                                                                 316 LVTCRVVHEALPGSRTLEKSLHYSAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: CARLY. CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211
TELECOMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEPHONE: (908) 594-6734
INFORMATION FOR SEQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
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amino acid
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Best Local Similarity 56.7<sup>3</sup>
Matches 185; Conservative
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PCT-US95-13795-2
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KQEGKVT-STHSELNIIQGEWVSQKTYTCQVTYQGFTFEDHARKCTESDPRGVSTYLSPP 290
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APPLICANT: Karasuyama, Hajime
APPLICANT: Karasuyama, Hajime
APPLICANT: Yonekawa, Hiromichi
APPLICANT: Taya, Choji
APPLICANT: Taya, Choji
TITLE OF INVENTION: Transgenic Animal Allergy Mod
TITLE OF INVENTION: Transgenic Animal Allergy Mod
TITLE OF INVENTION: Transgenic Animal Allergy Mod
CURRENT APPLICATION NUMBER: US/09/192,545
CURRENT FILING DATE: 1998-11-13
EARLIER FILING DATE: 1998-11-14
SERLIER PILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                       316 LVTCRVVHEALPGSRTLEKSLHYSAG 341
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Best Local Simi
Matches 147;
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Patent No. 6573372

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: McCall, Catherine

APPLICANT: Weber, Eric

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

FILE RPERENCE: P-1047

CURRENT APPLICATION NUMBER: US/09/479,614

CURRENT APPLICATION NUMBER: US/09/479,614

CURRENT PILING DATE: 1999-01-07

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATENTIN Ver. 2.0

SEPTIAND OF SECTION OF SECTION NUMBER: 05-01-07

NUMBER OF SECTION NUMBER: 05-01-07

SOFTWARE: PATENTING DATE: 1999-01-07

SOFTWARE: PATENTING DATE: 1999-01-07
     E Molecules and Related Methods
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 FILE OF INVENTION: Feline Immunoglobulin E P FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 2
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                                                                                                                                                                                                                                      Query Match 52.4% Best Local Similarity 56.7% Matches 185; Conservative
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Best Local Similarity 56.7%
Matches 185; Conservative
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Models and Methods for Their Use
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                                                    349
                                                                                                                                            256 TCLIRGFYPSEISVOWLFNNEEDHTGHHTTTRPOKDHGTDPSFFLYSRMLVNKSIWEKGN 315
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197
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                                 SPLDLYVHKSPKITCLVVDLANTDGMI-LTWSRENGESVHPDPMVKKTQYNGTITVTSTL
SPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTL
                                                                                                              PVGTRDWIEGETYOCRVTHPHLPRALMRSTTKLPGKRLAPEVYM-LPPSPE-ETGTTRTV
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llarity 41.6%; Pred. No. 1e-56;
Conservative 53; Mismatches 133; Indels
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PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR PLING DATE: 192-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
SEQ ID NO 1
LENGTH: 109
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Patent No. 6685939
GENERAL INFORMATION:
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; Sequence 1, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
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Best Local Similarity 97.2%;
Matches 106; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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    US-US-232-539D-56

Sequence 56, Application US/08232539D
Patent No. 5965709
GENERAL INFORMATION:
TITLE OF INVENTION: 1gE Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STRATE: Genentech, Inc.
STRATE: 1 DNA MAY
CITY: South San Francisco
STRATE: 1 DNA MAY
CITY: South San Francisco
STRATE: 1 DNA MAY
CITY: South San Francisco
STRATE: 1 DNA MAY
CONPUTER READABLE FORM:
MEDIUM TYPE: 35 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: STRATE: US/08/232,539D
APPLICATION NUMBER: US/08/232,539D
FILING DATE: 13-Apr-1994
CLASSIFICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION NUMBER: 07-JAN-1994
PRIOR APPLICATION NUMBER: 07-JAN-1994
PRIOR APPLICATION NUMBER: 07-JAN-1994
APPLICATION NUMBER: 07-JAN-1994
PRIOR APPLICATION NUMBER: 07-JAN-1994
TILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: SVODGG, CALAGG
RECISTRATION NUMBER: 99,044
REFERENCE/DOCKET NUMBER: 99,044
REFERENCE/DOCKET NUMBER: POT18P3
TELEFAX: 650/952-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 579; DB 2;
Pred. No. 1.3e-48;
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Patent No. 632509
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Pennard
ITLE OF INVENTION: Immunoglobulin Variants
FILE REPERENCE: P0718P2C1D1
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION WUMBER: US 08/405,617
PRIOR APPLICATION WUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/405,617
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INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
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Amino Acid
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Best Local Similarity 98.2
Matches 109; Conservative
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US-08-466-163B-1
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APPLICANT: Jardieu, Paula M.
APPLICANT: Dardieu, Paula M.
APPLICANT: Presta, Lecnard G.
ITITE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended); FILE REFERENCE: PO718P2C3US
CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT APPLICATION NUMBER: US/08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR PLING DATE: 1995-08-14
PRIOR PLING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US/07/44,768
PRIOR APPLICATION NUMBER: US/07/744,768
PRIOR PLING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NOS: 64
                                                                                                                                    124 DSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNJTWSRASGKPVNHSTRKE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 DSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKE 183
                                                                                                                                                                            1 DSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKE 60
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲,
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                                                                                                                                                                                                                                                                                                                       61 EKQRNGTLITVISTLPVGTRDWIEGET-QCRVTHPHLPRALMRSTTKTSG 108
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Query Match 29.6%; Score 548.5; DB 3; Length 109; Best Local Similarity 97.2%; Pred. No. 1.1e-45; Matches 106; Conservative 0; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 548.5; DB 4; Length 1
Pred. No. 1.1e-45;
0; Mismatches 2; Indels
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TOPOLOGY: Linca 232.
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US-08-232-539D-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 DSNPRGVSAYLSRPSPPDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMITTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,539D

FILING DATE: 1.4pr-1994

CLASSIFICATION NAMBER: 08/178583

FILING DATE: 07-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/744768

FILING DATE: 14-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: SOCODERA Craig G.
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.6%; Score 548.5; DB 4
Best Local Similarity 97.2%; Pred. No. 1.1e-45;
Matches 106; Conservative 0; Mismatches 2
                       CURRENT APPLICATION NUMBER: US/09/802,077
CURRENT APPLICATION NUMBER: US/09/802,077
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1995-03-15
PRIOR PILING DATE: 1994-01-26
PRIOR PILING DATE: 1992-01-26
PRIOR PILING DATE: 1992-01-14
PRIOR PILING DATE: 1992-06-14
PRIOR PILING DATE: 1992-06-14
PRIOR PILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
NUMBER OF SEQ ID NOS: 64
TYPE: PRI
CORGANISM: HOMO SADIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-232-539D-54

Sequence 54 Application US/08232539D

Sequence 54 Application US/08232539D

GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: 1gE Antagonists
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genertech, Inc.
STREET: I DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/22-1489
TELEPAX: 650/922-9881
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
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RESULT 12
US-09-820-995B-38
Sequence 38, Application US/09828995B
Sequence 38, Application US/09828995B
Retent No. 6703360
GENERAL INFORMATION:
APPLICANT: Heska Corporation
APPLICANT: McCall, Catherine A.
APPLICANT: Tang, Liang A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE 1gG AND CANINE IL-13 in TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE 1LCATION NUMBER: US/09/828,995B
CURRENT APPLICATION NUMBER: 06/195,874
PRIOR PILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-04-07
SPRIOR PILING DATE: 2000-04-07
SOFTWARE PREDENTING VERSION 3.1
SEQ ID NO 38
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 LTSGVHTFPSVL----QSSGLYSLSSTVTVPSSRW-PSETFTCNVVHPASNTKVDKPVFK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 GVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 -QEAENLFPYTTRPKREGGOTFSLOSEVNITQGQWMSSNTYTCHVKHNGS-----IFE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 DSSRKCADSNP-----RGVSAYLSRPSPFDLF-IRKSPTITCLVVDLAPSKGTVNLTWSR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 LPGKRLAPEVYMLPPSPEE--TGTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 HHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 ASGKPVNHS-TRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POKDHGTDPSFFLYSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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     Length 106;
                                                                                                                                                                                                             189 GILIVISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPG 232
                                                                                                                                                                                                                                        2; Indels
  Score 538; DB 2;
Pred. No. 1.1e-44;
0; Mismatches 2;
Query Match
Best Local Similarity 98.1%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
, ORGANISM: Canis familiaris
US-09-828-995B-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 36.4 Matches 129; Conservative
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US-09-828-995B-11
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195 -QSSGLHSLSSMVTVPSSRW-PSETFTCNVVHPASNTKVDKPVFNEC--RCTDTPPCPVP 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---RGVSAYLSRPSPFDLF-IRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHS-TRK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 BEKORNGTLIVISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTIKLPGKRLAPEVYML 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPSPEETGTTRIV--TCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 PPSPKELSSSDIVSITCLIKDFYPPDIDVEWQSNGQQEPERKGHRMIPPQLDE--DGSYFL 427
                                                                                                                                                                                                        23 PTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPK
                                                                                                                                                                                                                                               79 REGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGS-----IFEDSSRKCADSNP----
                                                                                                                                         Gaps
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APPLICANT: KINACHI, KAZUHIKO
APPLICANT: ONO, YOICHI
APPLICANT: ONO, YOICHI
APPLICANT: ONO YOICHI
TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
TITLE OF INVENTION: IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                         38;
                                                                         Length 468;
                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   428 YSKLSVDKSRWQQGDPFTCAVMHETLQNHYT-DLSLSHSPG 467
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                                                                  27.6%; Score 513; DB 4; L
36.4%; Pred. No. 2.8e-41;
ive 58; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,981
FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/08646981 Patent No. 5852183 GENERAL INFORMATION: APPLICANT: MAEDA, HIROAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32,181
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ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S
REGISTRATION NUMBER: 32,18
REFERENCE/DOCKET NUMBER: 1
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 334 amino acids
amino acid
                                                                                                      Best_Local Similarity 36.4%
Matches 124; Conservative
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          JS-09-828-995B-5
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                                                                         Query Match
Best Local
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Patent No. 6703360

GENERAL INFORMATION

APPLICANT: Heska Corporation

APPLICANT: Tang, Liang A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IL-13 R

FILE REFERENCE: AL-7

CURRENT FILING DATE: 2001-04-09

PRIOR PLILONG DATE: 2000-04-07

PRIOR PLILONG DATE: 2000-04-07

PRIOR PLILONG DATE: 2000-04-07

PRIOR PLILONG DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 104

SOFTWARE: Patentin version 3.1

SEQ ID NO SEC ID NOS: 104

SEQ ID NO SEC ID NOS: 104
                                                                                               APPLICANT: Heska Corporation
APPLICANT: Heska Corporation
APPLICANT: McCall, Catherine A.
APPLICANT: ACCALL Catherine A.
APPLICANT: Tang, Liang A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE 1gG AND CANINE IL-13 F
PILE REPRENCE: AL-7
CURRENT APPLICATION NUMBER: 05/195,874
PRIOR APPLICATION NUMBER: 60/195,874
PRIOR APPLICATION NUMBER: 60/195,659
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEC ID NOS: 104
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGS----- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 LTSG---VHTFPSVL----QSSGLYSLYSTVTVPSSRW-PSETFTCNVVHPASNTKVDKP 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 HWGNGTSLFVSSASTTAPSVFPLAPSCGSTSG---STVALACLVSGYFPEPVTVSWNSGS 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 TTKLPGKRLAPEVYMLPPSPEE--TGTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHT 284
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28.0%; Score 519.5; DB 4; Length 4
Best Local Similarity 36.4%; Pred. No. 6.5e-42;
Matches 130; Conservative 58; Mismatches 134; Indels
Sequence 11, Application US/09828995B
Patent No. 6703360
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Canis familiaris
US-09-828-995B-11
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ORGANISM: Canis familiaris
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US-09-828-995B-5
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LENGTH: 470
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                                                                                                                                                                                                                                                                                                                                                           |:| | | : | : | | | | : | | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                              23 PTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPK 78
Query Match 27.6%; Score 512; DB 2; Length 334;
Best Local Similarity 35.9%; Pred. No. 2.1e-41;
Matches 123; Conservative 60; Mismatches 122; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 FLYSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
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Search completed: November 14, 2004, 15:03:00 Job time : 40 secs

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1772
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1856
1 EFHHHHHHHLLSLPESGPVTI.......HEALPGSRTLEKSLHYSAGN 342
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1: \cgn2_6/ptodata/1/pubpaa/PCT_REW_PUB.pep:*
2: \cgn2_6/ptodata/1/pubpaa/PCT_REW_PUB.pep:*
3: \cgn2_6/ptodata/1/pubpaa/PCT_REW_PUB.pep:*
4: \cgn2_6/ptodata/1/pubpaa/NCSO_NEW_PUB.pep:*
5: \cgn2_6/ptodata/1/pubpaa/NCSO_NEW_PUB.pep:*
6: \cgn2_6/ptodata/1/pubpaa/NCSO_NEW_PUB.pep:*
7: \cgn2_6/ptodata/1/pubpaa/NCSO_NEW_PUB.pep:*
8: \cgn2_6/ptodata/1/pubpaa/NCSO_PUBCOMB.pep:*
7: \cgn2_6/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*
9: \cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
10: \cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
11: \cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
12: \cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
13: \cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
14: \cgn2_6/ptodata/1/pubpaa/USIO_PUBCOMB.pep:*
15: \cgn2_6/ptodata/1/pubpaa/USIO_PUBCOMB.pep:*
16: \cgn2_6/ptodata/1/pubpaa/USIO_PUBCOMB.pep:*
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                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		*				
		Query				
S	Score	Match	Match Length DB	DB	CI.	Description
	1856	100.0	342	6	US-09-401-636-8	Sequence 8, Appli
	1856	100.0	342	14	US-10-176-664-8	Seguence 8, Appli
	1856	100.0	342	72	US-10-673-594-8	œ
	1786	96.2	338	15	US-10-438-794-6	Sequence 6, Appli
	1786	96.2	338	15	US-10-453-915-6	Seguence 6, Appli
	1786	96.2	347	15	US-10-438-794-14	Sequence 14, Appl
	1786	96.2	347	15	US-10-453-915-14	14,
	1772	95.5	557	15	US-10-438-794-12	12,
	1772	95.5	557	15	US-10-438-794-16	16,
	1772	95.5	557	15	US-10-453-915-12	12,
	1772	95.5	557	15	US-10-453-915-16	16,
	1772	95.5	566	15	US-10-438-794-10	10,
	1772	95.5	566	15	US-10-438-794-18	

61 LVDGQEAENLFPYTTRFKREGGQTFSLQSEVNITQGQ#MSSNTYTCHVKHNGSIFEDSSR 120

61 LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNITQQQMMSSNTYTCHVKHNGSIFEDSSR 120

KCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHST 180

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8 8 8 8

Sequence 10, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 10, Appli Sequence 10, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 6, Appli Sequence 5, Appli Sequence 7, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 8, Appli Sequence 9, Appli Sequence 7, Appli Sequence 7, Appli	⋄	Length 342; Indels 0; Gaps 0; TIQLLCLVSGFSPAKVHVTW 60 TIQLLCLVSGFSPAKVHVTW 60
2 5 5 5 6 15 US-10-453-915-10 2 95.5 5 6 15 US-10-453-915-10 3 88.6 341 14 US-10-453-915-13 5 88.6 341 14 US-10-176-664-11 5 88.6 341 15 US-10-176-664-11 5 85.5 341 14 US-10-176-664-3 5 85.5 341 14 US-10-176-664-3 5 85.5 345 19 US-09-401-656-10 5 85.5 345 19 US-09-401-656-4 5 85.5 345 19 US-10-176-664-10 5 85.5 345 14 US-10-176-664-10 5 84.5 345 19 US-09-401-656-4 5 84.5 341 14 US-10-176-664-9 5 84.5 341 14 US-10-176-664-9 5 83.7 341 15 US-10-176-664-9 5 83.7 341 14 US-10-176-664-9 5 83.7 341 14 US-10-176-664-9 5 83.7 341 15 US-10-176-664-9 5 83.7 341 14 US-10-176-664-6 5 82.4 341 14 US-10-176-664-6 5 82.4 341 14 US-10-176-664-5 6 82.4 341 15 US-10-176-664-5 6 82.4 341 14 US-10-176-664-5 6 82.4 341 14 US-10-176-664-5 6 82.4 342 15 US-10-1638-794-8 6 80.1 555 15 US-10-438-794-8 6 80.1 555 15 US-10-438-794-8 6 69.3 44.3 14 US-10-1638-794-7 5 56.6 34.3 14 US-10-1638-794-7 5 56.6 34.3 14 US-10-1638-794-7	### Proprocession US/09401636 ### Papplication US/09401636 ### ### Papplication US/09401636 ### ### ### Papplication	Similarity 100.0%; Score 1856; DB 9; 2; Conservative 0; Mismatches 0; EFHHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHS
114 1172 116 1172 118 118 119 119 119 119 119 119 119 119	RESULT 1 US-09-401-636- Sequence 8, Patent No. U GENERAL NO. U GENERAL APPLICANT: TILLE OF IN FILE REFREE CURRENT APP CURRENT APP CURRENT APPLI PRIOR FILIN PRIOR FILIN NUMBER OF S SOFTWARE: SEQ ID NO 8 LENGTH: 34 LENGTH:	Query Match Best Local S Matches 342 Qy 1

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121
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                                                                                                    241 MLPPSPEETGTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
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                                                                                                                                                                                                                                                                               Sequence 8, Application US/10176664

PUBLICATION NO. US20030031663A1

GENERAL INFORMATION:

APPLICANT: Hellman, Lars T.

TILLE OF INVENTION: ENHANCED VACCINES

FILE REFERENCE: 10223/00601

CURRENT APPLICATION NUMBER: US/10/176,664

CURRENT APPLICATION NUMBER: US/09/401,636

PRIOR FILING DATE: 1999-09-22

PRIOR FILING DATE: 1999-09-22

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FASTERO for Windows Version 4.0

SEQ ID NO 8

LENGTH.
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APPLICANT: LUNDGREN, Mats
APPLICANT: FUENTES, Alexis
APPLICANT: FUENTES, Alexis
APPLICANT: FUENTES, Alexis
TITLE OF INVENTION: Continueric IgE Polypeptides and Host Cells
TITLE OF INVENTION: 10223-01701
GURRENT APPLICATION NUMBER: US/10/438,794
CURRENT FILING DATE: 2003-05-15
PRIOR APPLICATION NUMBER: US 60/382,552
PRIOR APPLICATION NUMBER: US 60/382,552
PRIOR FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 338
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 342;
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, OTHER INFORMATION: Synthetic polypeptide designated OSO
US-10-438-794-6
                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
02-10-673-594-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 1856; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-139;
Matches 342; Conservative 0; Mismatches 0;
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: BRHANCED
CURRENT APPLICATION NUMBER: US/10/673,594
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR PILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR PILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Length 338;

DB 15;

96.2%; Score 1786;

Query Match

Sequence 8, Application US/10673594 Publication No. US20040076625A1 GENERAL INFORMATION:

US-10-673-594-8

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EETGTTRIVICLIRGEVPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRN 188
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APPLICANT: LUNDGRRN, Mats
APPLICANT: PUENTES, Alexis
FAPLICANT: MEGNISSON, Ann-Christin
TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
FILE REFERENCE: 10223-017001
CURRENT APPLICATION NUMBER: US,10,438,794
CURRENT FILING DATE: 2003-05-15
PRIOR APPLICATION NUMBER: US,60/382,552
FRIOR FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 347;
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; OTHER INFORMATION: Synthetic polypeptide designated OSO-H
US-10-438-794-14
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                                                          NKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
                                                                              NKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 338
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Pred. No. 5.9e-134;
0; Mismatches 0;
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Sequence 14, Application US/10453915

Publication No. US20040054146A1

GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
APPLICANT: Jansson, Stefan
APPLICANT: Jansson, Asa
TITLE OF INVENTION: Allergy Vaccines
FILE RFFERENCE: 10223-008001

CURRENT APPLICATION NUMBER: US/10/453,915

CURRENT FILING DATE: 2003-06-02
                                                                                                                                                                                       Sequence 14, Application US/10438794; Publication No. US20040038395A1; GENERAL INFORMATION:
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Matches 334; Conservative
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US-10-438-794-14
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                                                                                                                                 69 NIFPYTTRPKREGGOTFSLOSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRKCADSNPR 128
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                                                      9 TLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAE
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                      Gaps
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                    Indels
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                      0
  No. 5.7e-134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-10-453-915-6
Squence 6, Application US/10453915
Publication No. US20040054146A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
APPLICANT: Perseson, Stefan
TITLE OF INVENION: Asa
FILE REFERENCE: 10223-008001
CURRENT APPLICATION NUMBER: US/10/453,915
CURRENT APPLICATION NUMBER: US/10/453,915
CURRENT FILING DATE: 2003-06-02
PRIOR FILING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 338
                    Mismatches
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  Pred.
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ORGANISM: Artificial Sequence
FEATURE:
99.48;
                Matches 334; Conservative
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Best Local Similarity
Matches 334; Conserv
Best Local Similarity
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                                                                       TLIVISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPEET 249
LFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 129
                    285 LFPYTTRPKREGGQTFSLQSEVNITQGQMMSSNTYTCHVKHNGSIFBDSSRKCADSNPRG 344
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US-10-438-794-16
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Pred, No. 1.4e-132;
2; Mismatches 3;
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Best Local Similarity 98.5%;
Matches 328; Conservative
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ORGANISM: Artificial Seguence
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US-10-438-794-16
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APPLICANT: LUNDGER, Mats
APPLICANT: FUENTES, Alexis
APPLICANT: FUENTES, Alexis
APPLICANT: FUENTES, Alexis
APPLICANT: PUENTES, Alexis
APPLICANT: POST Alexis
APPLICANT: MAGNUSSON, Ann-Christin
FILE REFERRNCE: 1023-017001
CURRENT APPLICATION NUMBER: US/10/438,794
CURRENT FILING DATE: 2003-05-15
PRIOR APPLICATION NUMBER: US 60/382,552
PRIOR FILING DATE: 2002-05-21
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                               Query Match 96.2%; Score 1786; DB 15; Best Local Similarity 99.4%; Pred. No. 5.9e-134; Matches 334; Conservative 0; Mismatches 0;
    PRIOR APPLICATION NUMBER: 60/408,648
PRIOR FILING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 14
LENGTH: 347
                                                                                                                                        OTHER INFORMATION: chimeric polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/10438794 Publication No. US20040038395A1 GENERAL INFORMATION:
                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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LENGTH: 557
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US-10-438-794-10

is Sequence 10, Application US/10438794

i Publication No. US20040038395A1

i Publication No. US20040038395A1

i APPLICANT: LUNDGREN, Mats

APPLICANT: LUNDGREN, Mats

APPLICANT: LUNDGREN, Ann-Christin

TILE OF INVENTION: Chimeric IgE Polypeptides and Host Cells

TILE OF INVENTION: Chimeric IgE Polypeptides and Host Cells

CURRENT APPLICATION NUMBER: US/10/438,794

CURRENT FILING DATE: 2003-05-15

FRIOR PAPLICATION NUMBER: US 60/332,552

PRIOR FILING DATE: 2002-05-21

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                Query Match 95.5%; Score 1772; DB 15; Best Local Similarity 98.5%; Pred. No. 1.4e-132; Matches 328; Conservative 2; Mismatches 3;
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llarity 98.5%; Pred. No. 1.4e-132;
Conservative 2; Mismatches 3;
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                                               ) OTHER INFORMATION: chimeric polypeptide US-10-453-915-16
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 328; Conserv
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LENGTH: 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                             APPLICANT: Hellman, Lars T.
APPLICANT: Persson, Stefan
APPLICANT: Persson, Stefan
APPLICANT: Persson, Asa
APPLICANT: Jansson, Asa
FILE REFERENCE: 10223-008001
CURRENT APPLICATION NUMBER: US/10/453,915
CURRENT FILING DATE: 2003-06-05
PRIOR APPLICATION NUMBER: 60/408,648
PRIOR PLING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 557
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US-10-453-915-16
Sequence 16, Application US/10453915
PUblication No. US20040054146A1
GENERAL INFORMATION:
APPLICANT: Hellnan, Lars T.
APPLICANT: Persson, Stefan
TITLE OF INVENTION: Allergy Vaccines
FILLE REFRENCE: 10223-008001
CURRENT FILLOR DATE: 2003-06-02
PRIOR PILLOR DATE: 2002-09-05
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 557
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: chimeric polypeptide
                                                              Sequence 12, Application US/10453915
Publication No. US20040054146A1
GENERAL INFORMATION:
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Best Local Similarity 98.55
Matches 328; Conservative
                    ULT 10
10-453-915-12
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APPLICANT: Jansson, Asa
TITLE OF INVENTION: Allergy Vaccines
FILE REFERENCE: 10223-00801
CURRENT APPLICATION NUMBER: US/10/453,915
CURRENT FILING DATE: 2003-06-02
PRIOR FILING DATE: 2003-09-05
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 566
                                                                                                                                                                                                                                                                                           OTHER INFORMATION: chimeric polypeptide
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LENGTH: 566
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                              250 GTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKS 309
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APPLICANT: FURBRES, Alexis
APPLICANT: FURBRES, Alexis
APPLICANT: FURBRES, Alexis
APPLICANT: MAGNUSSON, Ann-Christin
TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
CURRENT APPLICATION NUMBER: US/10/438,794
CURRENT FILING DATE: 2003-05-15
PRIOR FILING DATE: 2003-05-21
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastESQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 566;
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US-10-438-794-18
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US-10-438-794-18
Sequence 18, Application US/10438794
Publication No. US20040038395A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                  10 LSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAEN
                                                                                                                                                225 IDIPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAEN
                                                                                                                                                                                                                                                                                                                                                                                                         190 TLIVISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTIKLPGKRLAPEVYMLPPSPEET
                                                Gaps
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0
  Length 566;
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                                                  Indels
Query Match 95.5%; Score 1772; DB 15; Best Local Similarity 98.5%; Pred. No. 1.4e-132; Matches 328; Conservative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1772; DB 15;
Pred. No. 1.4e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 IWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
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Sequence 18, Application US/10453915
Sequence 18, Application US/10453915
Publication No. US20040054146A1
SEDERAL INFORMATION:
APPLICANT: Hellman, Lars T.
APPLICANT: Persson, Stefan
APPLICANT: Jansson, Asa
ITILE OF INVENTION: Allergy Vaccines
FILE REFERENCE: 10223-008001
CURRENT APPLICATION NUMBER: 607408,648
PRIOR APPLICATION NUMBER: 607408,648
PRIOR PELING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
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98.5%;
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ORGANISM: Artificial Sequence
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Best Local Similarity
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sequence 10, Application US/10453915; Publication No. US20040054146A1; GENERAL INFORMATION: APPLICANT: Hellman, Lars T.

RESULT 14 US-10-453-915-10

8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	LSLPESGPUTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWIVDGQBAEN 69	IDIPESGPUTIIPPTVKLFHSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAEN 284	LFPYTTREKGGOTFSLOSEVNITOGOMMSSNIYICHVKHNGSIFEDSSRKCADSNPRG 129	LFPYTTRPKREGGGTFSLQSEVNITGGGMMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG 344	VSAYLSRPSPPLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNG 189	VSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGRPVNHSTRKEEKQRNG 404	TLIVISTLEVGTRDWIEGETYQCRVTHPHLERALMRSTIKLEGKRLAPEVYMLEPSEET 249	TLTVISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTASPGKRLAPEVYMLPPSPEET 464	GTTRIVTCLIRGEYPSELSVOWLFNNEEDHTGHHTTTRPOXDHGTDPSFFLYSRMLVNKS 309	GTTRIVICLIRGEYPSEISVOMLENNEEDHIGHHTTTRPOKDHGTDPSFFFYSRMLVNKS 524	IMEKGNIVTCRVVHEALPGSRTLEKSLHYSAGN 342	I WEKGNLVICRVVHEALPGSRTLEKSLHYSAGN 557	
	SLPESGP	DIPESGP	FPYTTRP	FPYTTRP	SAYLSRPS	SAYLSRPS	TTVTSTLE	LTVTSTLE	TTRTVTCI	TTRTVTCI	WEKGNLVI	WEKGNLVI	
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Matches	δ	q	<i>λ</i> 0	qq	٥٨	qc	. V O	qq	δλ	Dþ	٥٠	Db	`

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November 14, 2004, 14:55:22; Search time 40 Seconds (without alignments) 822.653 Million cell updates/sec
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1 EFHHHHHTLSLPESGPVTI......HEALPGSRTLEKSLHYSAGN 342
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1: pir1:*
2: pir2:*
3: pir4:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	iσ	ь	b	b	Ig epsilon chain C	g epsilon cha	g Y heavy cha	g gamma ch	g mu chain C	g mu chain C	q mu chain C	g gamma-2	g mu chain C	g gamma-4 cha	g mu chair	g gamma 3	יט	g mu chain	g mu chain	g mu	g gamma 2b	g gamma 2a	b	g heavy cha	יט	o mur	g mu chain -	g gamma-1 chai	Ig mu chain C regi
	DI	БННО	I36948	EHRT	EHWS	S38864	EHWSS	B46529	800390	MHRBM	MHHY	MHRB	G2HU	525644	G4HU	S14683	147161	831436	MHMS	A24976	MHMSM	147160	I47159	837768	1559	147158	MHHUBT	0	GHHO	MHHU
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453.5	450	447	447	447	446.5	444	443.5	440	437.5	437.5	436.5	429	428	428	424.5
4															

ALIGNMENTS

	RESULT 1
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	Ig epsilon chain C region - human
	C;Species: Homo sapiens (man)
	C;Date: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
	C; Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C4
	R;Flanagan, J.G.; Rabbitts, T.H.
	EMBO J. 1, 655-660, 1982
	A; Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gen
	A; Reference number: A22771; MUID:84236029; PMID:6234164
	A;Accession: A22771
	A; Modecule type: DNA
	A, Cross-reigrences: UNIPROT: P01854; GB: L00022; GB: U00527; GB: V00555; NID: 9185035
	K'Ueda, b.; Nakal, b.; NISDIDa, Y.; HISAJIMA, H.; HONJO, T.
	DANDO U. 1, 1939-1934; 1998 A. Wittou Tong thomas 1 1998
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••••	A:Cross-reference: GR-10022: NID-0184755
•••	D. Chang K. Caver D. Max F. F. Caver D. Max F. F. Caver D. Max F. F. Caver D. Max F. F. Caver D. Caver
	Exp. Med 176 0.23 - 24 1992
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	A)CLOSS-IELECTECTORS: EMBLIA03039; GELSOOGOGO; NILUGUZZGO) P.CEDO M. KITCKEWS T. ONO V. Onda H. Gaesda D. Trazachi K. Kibuchi M. Gur
	A. I. KINGGIL, H.,
	Nuclear Actua Res. II., /IJ-/Ze, IJ00. Nuclear Actua Res. II., /IJ-/Ze, IJ00. Nuclear Actual Res. II., /IJ-/Ze, IJ00.
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	R.Max. E.E. Harttev. J. v. Nav. R. F. Kirsch. T. R. J. Jeden. D.
	Cell 29, 691-699, 1982
	A, Title: Duplication and deletion in the human immunoglobulin epsilon genes.
	A; Reference number: A90824; MUID: 83001945; PMID: 6288268
	A; Accession: A90824
	A; Molecule type: DNA
	A; Residues: 1-358, 'L', 360-428 < MAX>
	A;Cross-references: GB:J00222; NID:g184755
	A; Note: this sequence difference may be due to polymorphism
	in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-
-	A; Kelerence number: A94418
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A; Residues: 'GAWTL', 6, 'X', 8-16, 'B', 18-43,'B', 45-52,55-92,95-97,'B',99-121,'B',123,'L',12 A; Experimental source: myeloma protein Nd R; Kanten, J. H.; Molgatad, H.V.; Audificon, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G Proc. Natl. Acad. Sci. U.S.A. '79, 6661-6665, 1982
A; Title: Cloning and sequence determination of the gene for the human immunoglobulin eps A; Reference number: A93933; MulD:83065234; PMID:681565
A; Accession: B9333
A; Molecule type: mRNA
A; Residues: 1-40;68-114;427-428 < KEN>
A; Cross-references: GB:L00022; NID:g185035
B; Rikeyam, S.
FEBS Lett. 234, 306-310, 1987
A; Residues: 1-40;68-114;427-428 < KEN>
A; Reference number: S02438; MUD:88083554; PMID:3121387
A; Reference number: S02438; MUD:88083554; PMID:3121387
A; Residues: 100-161c acid sequence not shown
A; Molecule type: mRNA
A; Residues: 98-352 < IKE>
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A;Accession: C46536
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A;Accession: C46536
A;Accession: D452426
A;Experimental source: B call myaloma U-266
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Query Match Best Local Similarity

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RjSakoyama, Y.; Hong, K.
Proc. Natl. Acad. Scl. U.S.A. 84, 1080-1084, 1987
A;Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and oranguta
A;Reference number: 136948; MUID:87147196; PMID:3103123
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                                                                                                                                                                                                                                                                 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 ONFMPEDISVOWLHNEVQLPDARHSTTOPRKTKGS--GFFVFSRLEVTRAEWEQKDEFIC 405
                                                                                                                                                                                                                 201
                                                                                                                                                                                                                                                                                                                                                                                                                                  RGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKSIWEKGNLVTC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig epsilon-chain - chimpanzee (fragment)
Cispecies: Pan troglodytes (chimpanzee)
Cibte: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
Cibtesion: I36948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKORNGTLTVTSTLPVGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DWIEGETYQCRVTHPHLPRALMRSTIKLPGKRLAPEVYMLPPSPEETGT--TRTVTCLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRKCADSNPRGVSAYLSRPFPDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFYPSEISVOWLFUNEEDHIGHHTTTRPOKDHGTDPSFFLYSRMLVNKSIWEKGNLVTCR
PPIVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAENLFPYTTRPKREG
                               GQTFSLQSEVNITQGQMMSSNTYTCHVKHNGSIFEDSSRKCADSNPRGVSAYLSRPSPFD
                                                                                                                                         169 GELASTQSELTLSQXHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSRPSPFD
                                                                                                                                                                                                                                                                 229 LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGT
                                                                                                                                                                                                                                                                                                                        RDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPEETGT--TRTVTCLI
                                                                                                                                                                                                                                                                                                                                                                      289 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAF-ATPEWPGSRDKRTLACLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 PTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAENLFPYTTRPKREGG
                                                                                                                                                                                                                 LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKORNGTLTVTSTLPVGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-426 <RES>
A;Cross-references: GB:M15398; NID:g176797; PIDN:AAA35416.1; PID:g176798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 103/1; 209/1; 317/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;336-405/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.2%; Score 1024.5; DB 2; Length 61.7%; Pred. No. 8.4e-69; ive 42; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: 136948
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 RVVHEALPGSRTLEKSLHYSAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAVHEAASPSQTVQRAVSVNPG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 VVHEALPGSRTLEKSLHYSAG 341
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~Z.

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A, Moclecule type: mRNA
A, Residues: 1-388 <LIU>
A, Residues: 1-388 <LIU>
A, Cross-references: UNIPROT: P06336; GB: J00476; NID: g194875; PIDN: AAA38085.1; PID: g38722
C, Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C, Superfamily: immunoglobulin cregion; immunoglobulin homology
C, Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology (fragment) <IMI>
F; 18-44/Domain: immunoglobulin homology <IM3>
F; 18-6-254/Domain: immunoglobulin homology <IM3>
F; 290-361/Domain: immunoglobulin homology <IM3>
F; 200-361/Domain: immunoglobulin homology <IM4>
F; 10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.
A;Reference number: A02144; MUID:83117774; PMID:6818553
A;Accession: A02144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SASQWYTKHHNNATTSITSILPVVAKDWIEGYGYQCIVDHPDFPKPIVRSITKTPGQRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 DSSRKCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AHTRRCPDHEPRGVITYLIPPSPLDLYQNGAPKLTCLVVDLESEK-NVNVTWNQEKKTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FICHVIHPPSFNESRIILVRPVNITEPILELLHSSCDPNA-FHSTIQLYCFIYGHILNDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 HVTWLVDGQEAENLFPYTTRPKREGGQTFSLQSEVNITQGQMMSSNTYTCHVKHNGSIFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEVYMLPPSPEETGTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQXDHGTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 LPESGPVTIIPPTVKLFHSSCDPRGD--AHSTIQLLCLVSGFSPAKVHVTWLVDGQEAEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHHHHHHLSLPES-----GPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 14; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
36.7%; Score 682; DB 2; L
Best Local Similarity 43.0%; Pred. No. 3.6e-43;
Matches 142; Conservative 52; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                        40.5%; Score 751; DB 1;
44.8%; Pred. No. 1.7e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain LOU/c/Wsl, immunocytoma IR2
R;Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.
DNA 1, 335-343, 1982
A;Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, A;Reference number: A90937; MUID:83182019; PMID:6820340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Molecule type: mRNA
A.Residues: 'N',169-307,'L',309-342 <KIN>
A.Residues: 'N',169-307,'L',309-342 <KIN>
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kalbain disulfide bonds: In some cases, such as 18A and 19M, the subunits associate into 15.5uperfamily: immunoglobulin C region; immunoglobulin homology
C.Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F.118-486/Domain: immunoglobulin homology <IML>
F.128-21/Domain: immunoglobulin homology <IMS>
F.233-231/Domain: immunoglobulin homology <IM3>
F.327-388/Domain: immunoglobulin homology <IM3>
F.327-388/Domain: immunoglobulin homology <IM4>
F.46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 AQNVLIKEEGKLASTYSKLNITQQQMMSESTFTCKVTSQGENYWAHTRRCSDDEPRGVIT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIVICLIRGFYPSEISVQWLFNNEEDHIGHHTTIRPQKDHGIDPSFFLYSRMLVNKSIWE 312
                                                                                                                                                                                                                                                                                                   from rat immunoglobulin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 PVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAENLFPYTTR 76
                                                                                                                                                           Cispecies: Rattus norvegicus (Norway rat)
Cibate: 17-bec-1982 #sequence revision 17-bec-1982 #text_change 09-Jul-2004
Cibate: 17-bec-1982 #sequence revision 17-bec-1982 #text_change 09-Jul-2004
Cibacession: A93442, A90037; A02143
R;Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982
A;Fitle: Structure and evolution of the heavy chain from rat immunoglobulin
A;Reference number: A93442; MUID:83064537; PMID:6292865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig. epsilon chain C region (version 1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A02144
R;Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVNITKPTVDLLHSSCDPNA-FHSTIQLYCFVYGHIQNDVSIHWLMDDRKI-----YETH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.4%; Score 767.5; DB 1;
45.8%; Pred. No. 1.1e-49;
tive 54; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
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     AVHEAASPSQTVQRTVSVNPG 425
                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: mRNA
A,Residues: 1-429 <HEL>
A,Cross-references: UNIPROT:P01855
                                                                                                                                       chain C region - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 45.8%
                                                                                                                                                                                                                                                                                                                                                   A; Accession: A93442
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Ig gamma chain (clone 36) - chicken (fragment)
NAlternate names: 1g nu chain
C;Alternate names: 1g nu chain
C;Accesion: 800390
R;Parvari, R; Aviv, A; Lentner, F; Ziv, E; Tel-Or, S.; Burstein, Y.; Schechter, I.
EMBO J. 7, 739-744, 1988
A;Title: Chicken immunoglobulin gamma-heavy chains: limited VH gene repertoire, combinat
A;Reference number: S00390; MUID:88203642; PMID:3135182
                                                                                                                                                                                                                                                                                                                                                                                                               the duck, Anas platyrhynchos:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 VPPSPGSLYIRQDAKVHCLVVNL-PSDASLSISWTREKSGALRPDPWVLTBHFNGTFTAS 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GGQTFSLQSEVNITQGQWMSSNTYTCHVKH--NGSIFEDSSRKCADSNPRG---VSAYL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKSIWEK 313
                                                                                                                                                                   Ig Y heavy chain (7.85) - duck
N.Alternate names: Ig gamma chain (7.85)
C.Species: Anas platyrhynchos (domestic duck)
C.Species: Anas platyrhynchos (domestic duck)
C.Species: Anas platyrhynchos (domestic duck)
C.Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C.Accession: B46529; S20759
R.Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992
J. Immunol. 149, 2627-2633, 1992
A;Hitle: Structural relationship between the two IgY of the duck, Anas plat;
A;Reference number: A46529; MUID:93017865; PMID:1401901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 SRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKBEKQRNGTLTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 AGSKTYMATSQTNVSREDWKAGKAFTCRVKHPATGGTAQGHARFCPGSGAQSCSPIQIFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPTVKLFHSS-CDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAENLFPYTTRPKRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPEETGTTR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X65219; NID:g62442; PIDN:CAA46322.1; PID:g62443
A;Experimental source: spleen
A;Note: sequence extracted from NCBL backbone (NCBIP:116127)
C;Superfamily: immunoglobulin C region; immunoglobulin homology
365 KSNGSNQGFFIFSRLEVAKTLWTQRKQFTCQVIHEALQKPRKLEKTISTSLGN 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
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A;Residues: 1-504 <PAR>
A;Cross-references: EMBL:X07174
A;Note: this sequence was determined from the differentiated ger
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 31.3%; Score 580.5; DB 2; Best Local Similarity 38.2%; Pred. No. 1.4e-35; Matches 124; Conservative 56; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F,37-120/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNLVTCRVVHEALP---GSRTLEKS 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVSYACMVVHEGLPMRFTQRPLQKT 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Astatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-572 <MAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81
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A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Mote: the sequence was determined from the germline gene
C. Genetics: 91/1; 199/1; 307/1
C. Genetics: 91/1; 199/1; 307/1
C. Complex: An immunoglobulin heerotetramer subunit consists of two identical light (kap that disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C. Keywords: duplication: glycoprotein; hererotetramer; immunoglobulin
C. Keywords: duplication: glycoprotein; hererotetramer; immunoglobulin
F. 115-183/Domain: immunoglobulin homology <IRMI>
F. 120-288/Domain: immunoglobulin homology <IRMI>
F. 1212-181, 227-286, 332-394/Disulfide bonds: #status predicted
F. 133-75, 122-181, 227-286, 332-394/Disulfide bonds: #status predicted
F. 143, 84, 167, 239, 262, 417/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epsilon gene: comparison
                                                                            189
                                                                                                                       338 VITYLIPPSPLDLYQNGAPKLTCLVVDLESEK-NVNVTWNQEKKTSVSASQWYTKHHNNA 396
                                                                                                                                                                                                               249
                                                                                                                                                                                                                                                                                456
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                                                                                                                                                                                                                                                                                                                                                                                                                       516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSIFEDSSRKCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GKRLAPEVYMLPPSPEETGTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQ 289
       TLAQTVLIKEE-GKLASTCSKLNITEQQWMSESTFTCKVTSQGVDYLAHTRRCPDHEPRG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
EHMSS

EHMSS

(1) expecies: Mus musculus (house mouse)

(2) Species: Mus musculus (house mouse)

(3) Species: Mus musculus (house mouse)

(3) Species: Mus musculus (house mouse)

(3) Species: Mus musculus (house mouse)

(4) Species: Musculus (house mouse mouse (house of house)

(5) Accession: A02145

(6) Rishida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T.

(6) First (house mouse immunoglobulin epsilon gene: companies of the mouse immunoglobulin epsilon gene: companies (house mounder: Askeference number: 
                                                                                                                                                                                                                                                       TISITSITPVAKDWIEGYGYQCIVDHPDFPKPIVRSITKTPGQRSAPEVYVFPPPEEES
                                                                                                                                                                                                                                                                                                                                                                                             FICHVIHPPSFNESRIILVRPVI----HSLSPPWSYSIHRCDPNA-FHSTIQLYCFIYGH
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                                                                            VSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNG
                                                                                                                                                                                                               190 TLIVISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPEET
                                                                                                                                                                                                                                                                                                                                                     250 GITRIVICLIRGFYPSEISVQWLFNNEEDHIGHHITTRPQKDHGIDPSFFLYSRMLVNKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FHHHHHHILSLPESGPVTIIPPTVKLFHS-----SCDPRGDAHSTIQLLCLVSGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMEKGNLVTCRVVHEALPGSRTLEKSLHYS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 41.6
Matches 147; Conservative
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Ajintrons: 105/3; 218/3; 324/3
Ajintrons: 105/3; 218/3; 324/3
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kanal dishu disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1 C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;120-90/Domain: immunoglobulin homology < IRMI>
F;238-306/Domain: immunoglobulin homology < IRMI>
F;345-416/Domain: immunoglobulin homology < IRMI>
F;454-112,139,122,210,238,257,280,326,441/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chains: direct comparison of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Val and
                                                                                                                                                                                                                                       328 EVAKHPPAVYVLPPAREQLVLRESATVTCLVKGFSPADVFVQWQQRGQPLSSDKYVTSAP 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149
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                                                                       DS---SRKCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASG 173
                                                                                                                               211 KNVSMSSECSTTPSPGIQVFPIAPSFADTFLSKSARLICLVTDLT-TYGSLNISWASHNG 269
                                                                                                                                                                                             KPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGK 233
                                                                                                                                                                                                                                                                                                                     RLA---PEVYMLPPSPEE--TGTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRP 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mesocricetus auratus (golden hamster)
C;bates: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
C;bates: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
C;Accession: A02168
R;McGuire, K.L.; Duncan, W.R.; Tucker, P.W.
Nucleic Acids Res. 13, 5611-5628, 1985
A;Title: Phylogenetic conservation of immunoglobulin heavy chains: direct oc A;Reference number: A02168; MUID:85297761; PMID:2994005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 HHGNINKDLRVPIPG-VTEMNPNVSVFVPSRDAFSGPAPRKSRLFCEASNFSPKQITVSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                       QKDHGTDPSFFLYSRMLVNKSIWEKGNLVTCRVVHEALP---GSRTLEKSLHYSAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APEPQAPGLYFTHSTLIVTEEDWNSGETFICVVGHEALPHMVTERTVDKSTEGEVG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 HHHHT---LSLPESGPVTIIPPTVKLFHSSCDP-RGDAHSTIQLLCLVSGFSPAKVHVTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 NHSTRKEEKORNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPG-KRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 APEVYMLPPSPEE--IGTTRIVICLIRGFYPSEISVOWLFNNEEDHTGHHTTTRPQKDHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 PPAVYQQPLAREQLILRESATVTCLVKGFSPADIFVQWLQRGQPLSQDKYVTSAPMREPQ
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A;Residues: 1.454 <MCG
A;Note: the sequence was determined from the germline gene
A;Note: the authors translated the codon GGT for residues 105.
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llarity 34.5%; Pred. No. 2e-29;
Conservative 60; Mismatches 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mu chain C region - golden hamster
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Matches 119; Conserv
             151
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                                                                    10;
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                                                                                                                                                                      PVPPVAPEVQVLHASSCTP--SQSESVELLCLVTGFSPASAEVEMLVDG--VGGLLVASO 227
                                                                                                                                                                                                                                                    RPKREGGOTFSLOSEVNITOGOWMSSNTYTCHVKH--NGSIFEDSSRKCADS----NPRG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464
                                                                                                                                                                                                                                                                                                                                                                      VSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLIVISILPVGIRDWIEGETYQCRVTHPHLPRALMRSTIKLPGKRLAPEVYMLPPSPEET 249
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                                                                                                                                                                                                                                                                                           WLVDGQEAEN---LFPYTTRPKREGGGTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFE
                                                                                                                        PVTIIPPTVKLFH-SSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAENLFPYTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTR-TVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTTRPQKDH-----GTDPSFFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 HSNSNRDLRVSFPVDSELPPNVSVF---IPPRDSFSGSGTRKSRLICQATGFSPKQISVS
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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         Length 504;
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                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.8%; Score 497.5; DB 1; 32.9%; Pred. No. 1.6e-29; ive 61; Mismatches 153;
Query Match 28.9%; Score 535.5; DB 2;
Best Local Similarity 35.1%; Pred. No. 2.6e-32;
Matches 118; Conservative 56; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRMLVNKSIWEKGNLVTCRVVHEALP---GSRTLEK 334
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Best Local Similarity 32.9%
Matches 117; Conservative
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A; Gross-references: GDB:119338; 'CMIM:147110
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A; Gross-references: GDB:119338; 'CMIM:147110
A; Gross-references: GDB:119338; 'CMIM:147110
A; Gross-references: GDB:119338; 'CMIM:147110
A; Gross-references: GDB:119338; 'CMIM:147110
A; Gross-references: GDB:119338; 'CMIM:147110
C; Gross-references: GDB:119338; 'CMIM:150-14710; 'GDB:110-14710; 'GDB:11
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that shown in having 60-Ala and in the amidati
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A,Residues: 1-24, E',26-57, EV', 60-85,132-171, ZZZ',175, B',177-193, D',195-196,'Q',198-A,Note: this sequence has since been revised
R;Hofmentn, T.; Patr, D.M.
Mol. Immunol. 16, 923-925, 1979
                    A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; A;Note: Lys-326 is probably removed posttranslationally
R;Nang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: Mycloma protein Til
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin A; Reference number: A93132; MUID:80114419; PMID:118920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Reference number: A90752; MUID:80001357; PMID:113060
A,Contents: myeloma protein Zie
A,Mocession: A90752
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                                                                                                                                                                                                                                                                                                                                                                    A; Accession: Å92809
A; Molecule type: protein
A; Residues: 1-19, 'Q', 21-57, 'Z', 59,'A', 61-193,'D', 195-325 < WAN>
A; Residues: 1rp-156 is at or near the complement-binding site
R; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
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Biochem. J. 121, 217-225, 1971
A;Title: Disulphid bridges of the heavy chain of human immu A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
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Local Similarity 36.2%; Pred. No. 6.7e-29;
les 117; Conservative 57; Mismatches 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 238-275 + HOF>
R;HGmann, T; Parr, D.M.
submitted to the Atlas, March 1980
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A;Contents: annotation; Zie,
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G;Species: Homo sapiens (man)

CjSpecies: Homo sapiens (man)

C;Darcession: A93906; A92809; A90752; A93132; A02148

C;Accession: A93906; A92809; A90752; A93132; A02148

C;Accession: A93906; A92809; A90752; A93132; A02148

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con

A;Reference number: A93906; MUID:82197621; PMID:6804948

A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 HSNSNRDLRVSPPVDSELPPNVSVP---IPPRDSFSGSGTRKSRLICQATGFSPKQISVS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 KPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 RLA---PEVYMLPPSPEE--TGTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 KALDTHANITESHPNATFSAMGEASVCAEDWESGEOFTCTVTHADLPPPLKHTISK--SR 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HHHHILSLPESGPV-TIIPPTVKLFHSSCDPR----GDAHSTIQLLCLVSGFSPAKVHVT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 DS---SRKCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 APEPQAPGLYFTHSTLTVTEEDWNSGETFTCVVGHEALPHMVTERTVDKS 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 495.5; DB 1; Length 458; Pred. No. 2.2e-29; 61; Mismatches 148; Indels 25.
APHLYFTHSVLTVTEEEWNSGETYTCVVGHEALPHMVTERTVDRS 433
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Matches 116; Conservative
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                   IRGEYPSEISVOWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKSIWEKGNLVT 318
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                                                                                                                                                                                                                                                                                                                        .Species: Rattus norvegicus (Norvay rat)
.Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 21-Jan-2000
.Accession: S25644
                                                                                 14 GPAPRKSRLICEATNFSPKQITVSWLQDGKPVKSGFTTEPVTVEAKGSRPQTYKVISTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKBEKQRNGTLTVTSTLPV
                                                              GTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPEE-TGTTRTVTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 GDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAENLF---PYTTRPKREGGQTFSLQSEVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 SVOWLFINNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKSIWEKGNLVTCRVVHEALP
                                                                                                                                                                                                                                                                                                                                                                   A/ACCession: 6.25044
Submitted to the EMBL Data Library, September 1992
Submitted to the EMBL Data Library, September 1992
A/Reference number: 825644
A/Refeasion: 825644
A/Residues: 1-343 < PAR>
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A/Residues: 1-344-305/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.9%; Score 480.5; DB 2;
llarity 34.7%; Pred. No. 2e-28;
Conservative 59; Mismatches 131;
                                                                                                                                                                                                                  | |:|||| | CSVMHEALHNHYT-QKSLSLSPG 325
                                                                                                                                                                                             CRVVHEALPGSRTLEKSLHYSAG
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HMVTERTVDKS
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Best Local Similarity
Matches 108; Conserv
                             128
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Ig gamma-4 chain C region - human C;Species: Homo sapiens (man) C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004 C;Accession: A90933; A00549; A00150 R;Ellison, J.; Buxbaum, J.; Hood, L.

RESULT 14 G4HU

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A)Consolution: 14932.33-14932.33
A)Map position: 1401/11/12.21/1
C)Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l C)Superfamily: immunoglobulin cregion; immunoglobulin homology <IMJ-
E)20-85/Domain: immunoglobulin homology <IMJ-
E)39-110/Region: hinge
E)34-203/Domain: immunoglobulin homology <IMJ-
E)144-203/Domain: immunoglobulin homology <IMJ-
E)134-203/Domain: immunoglobulin homology <IMJ-
E)144/Disulfide bonds: interchain (to light chain) #status experimental
E)177/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Homo sapiens (man)
C;Dates: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C;Accession: 814683; 808047
R;Friadlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A;Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain A;Reference number: $14683; MUID:90332450; PMID:2115996
                                                                                                                                                                                                                                                                                                                                                                                                                             constant
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                                                                                                                                                                                                                                                                                                                                                                                                                     of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 RGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPKREGGQTFSLQSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 VGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPEE-TGTTRTVTC
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DNA 1, 11-18, 1981.

A,Title: Nuclectide sequence of a human immunoglobulin C-gamma4 gene A,Reference number: A90933; MUID:83157104; FMID:6299662.
A,Accession: A90933
A,Modecule type: DNA
A,Residues: 1-327 < ELL>
A,Cross-references: UNIPROT:P01861
A,Cross-reference was determined from the germline gene A,Ribink, J.R.L.; Buttery, S.H.; Do Vries, G.M.; Milstein, C. Biochem. J. 117, 33-47, 1970
A,Title: Human immunoglobulin sublclasses. Partial amino acid sequence A,Reference number: A90249; MUID:70207560; PMID:4192699
A,Accession: A90249
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A;Residues: 1-30;81-326 <PIN>
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A; Gene: GDB: IGHG4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 EKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRL-APEVYML 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428 ESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLL 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 PPSPEETG--TTRTVTCLIRGPYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 PVTII---PPTVKLFHSSCDPR----GDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAEN 69
                                                                                                                                                                                                                                               Query Match 25.6%; Score 475.5; DB 2; Length 627;
Best Local Similarity 31.4%; Pred. No. 9.9e-28;
Matches 106; Conservative 65; Mismatches 142; Indels 25; Gaps
A;Molecule type: mRNA
A;Residues: 1-627 <FRI>
A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin; membrane protein
F;11S/Domain: signal sequence #status predicted <SIG>
F;16-627/Product: Ig um chain #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
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P04221 oryctolagus
Camzu6 homo sapien
Cae45931 homo sapien
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1 EFHHHHHHTLSLPESGPVTI......HEALPGSRTLEKSLHYSAGN 342
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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BACB5440
EPC RAT
EPC MOUSE
MUCM RABIT
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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MUC MOUSE MUCM MOUSE

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MUC_HUMAN 07TMT6

Q86ttl homo sapien Q6pjfl homo sapien Aahl6381 homo sapi

Q8wux4 homo sapien Q5gmx5 homo sapien Q9bul0 homo sapien Q9bul0 homo sapien Q9bb9 homo sapien Q6gmy2 homo sapien Q6gmy2 homo sapien Q86a6 homo sapien Q96a6 homo sapien Q96a6 homo sapien Q96a7 homo sapien Bac8537 homo sapien Bac85202 homo sapien Bac85202 homo sapien Bac85202 homo sapien			rata; Euteleostomi; Inidae; Homo.	.R., Igarashi K., of human immunoglobulin	rr P.; globulin epsilon genes.";	epsilon heavy chain constant allelic genes.";	Honjo T.; human immunoglobulin	trom H.; d developments, pp.1-36,	A. cbyshire R.B., Viney J., gene for the human myeloma cell line.";
Q8WUX4 Q6GMX5 Q9BQB8 Q9BQB0 Q9BD10 Q96BD10 Q96MVX1 Q96AA6 BAC85387 AAH14667 MUCB HUMAN BAC85202 BAC85697	ALIGNMENTS	PRT; 428 AA. ed) sequence update) annotation update)	a, Craniata, Vertebrata 88, Catarrhini, Hominida	SEQUENCE FROM N.A. MEDLINE=8316887; PubMed=6300763; Seno M., Kurokawa T., Ono Y., Onda H., Sasada Kikuchi M., Sugino Y., Nishida Y., Honjo T.; "Molecular cloning and nucleotide sequencing cepsilon chain cDNA."; Nucleic Acids Res. 11:719-726(1983).	IANT LEU-359. 188268; Kirsch I.R., Leder n the human immunoglc	:34164; i.; munoglobulin epsilc or three non-alleli	MEDLINE-84207910; PubMed-6327276; MEDLINE-84207910; PubMed-6327276; Ueda S., Nakai S., Nishida Y., Hisajima H., Ho "Long triminal repeat-like elements flank a hu epsilon pseudogene that lacks introns.";	PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND). Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom (In) Bach M.K. (eds.); Immediate hypersensitivity: modern concepts and dev	427-428 FROM N 655; doughton M., Del nation of the expressed in a
255.1. 255.1. 255.1. 255.1. 255.1. 255.1. 257.2. 255.1. 257.2. 257.2. 257.2. 257.2. 257.2. 257.2. 257.3. 25		STANDARD; i (Rel. 01, Created) (Rel. 01, Last seqn (Rel. 45, Last anno	(Human) stazoa; Chordata; theria; Primates; 506;	4 N.A. 8897; PubMed=63 bkawa T., Ono Naghagian or Nish Contag and nucl	1 N.A., AND VAR 1945; PubMed=62 tey J., Ney R. and deletion i	1 N.A. SO29; PubMed=62 , Rabbitts T.F. s of a human in and evidence fi-660(1982).	I N.A. 1910; PubMed=63 ii S., Nishida Il repeat-like logene that lac 19-1544(1982).	PERLIMINARY SEQUENCE (MYELOWA Bennich H.H., Johansson S.G.O. (In) Bach M.K. (eds.); Immediate hypersensitivity; mo Marcel Dekker, New York (1978)	-40; 68-114 AND 234; PubMed=6815 Molgaard H.V., Puld H.J.; sequence determine epsilon chain
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Ig-like 2.
Ig-like 3.
Ig-like 4.
Interchain (with a light chain)
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                                                                                                                                                                                                                                                                                           W -> L (possible polymorphism). /FTId=VAR 003885.
                                                                                         Proc. Natl. Acad. Sci. U.S.A. 79:661-6658(1982).
[7]
MEDINE-BYRUCTURE MODELING.
MEDINE-87089848; PubMed=3796618;
Padlan E.A., Davies D.R.;
"A model of the Fc of immunoglobulin E.";
Mol. Immunol. 23:1063-1078(1986).
-:- SIMILARITY: Contains 4 immunoglobulin-like domains.
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BAC85440;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLU27315 fis, clone TMS06851, highly similar to Ig epsilon chain
C region.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primata; Catarrhini; Hominidae; Homo.
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                                             56.0%; Score 1038.5; DB 1; Length 428; 62.4%; Pred. No. 9.3e-72; ive 41; Mismatches 73; Indels 7;
47019 MW; 25C4CA072AA558A0 CRC64;
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Sciurognathi, Muridae, Murinae, Mus.
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Ig-like 3.

Ig-like 4.

Ig-like 4.

R -> N (in Ref. 2).

R -> L (in Ref. 2).

W, D2970B34EF8A72B0 CRC64;
(epsilon) chain of rat immunoglobulin E.";
Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
-!- SIMILARITY: Contains 4 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                       Immunoglobulin C region, Immunoglobulin domain, Repeat.
NON TER
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45.8%; Pred. No. 7.3e-51;
tive 54; Mismatches 114;
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P06336; P01856;
21-UUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
IG epsilon Chain C region.
Mus musculus (Mouse).
Bukaryota, Mertazoa; Chordata; Craniata; Vertebri Mammalia; Butheria; Rodentia; Sciurognathi; Mur.
NCBI_TAXID=10090;
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                                                                                                                                                                      EMBL, J00744, AAA41379.1; ALT_INIT.
PIR, A93442; EHRT.
HSSP, P01854; IFP5.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.c.
InterPro; IPR003506; Ig.MHC.
Pfam; PP0047; ig; 4.
PROSITE; PS0835; IGLIKE; 4.
PROSITE; PS0835; IGLIKE; 4.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.; "Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3] SEQUENCE OF 205-306 FROM N.A.
MEDLINE-82174576; PubMed=6803238;
Hellman L., Pettersson U., Bennich H.;
"Characterization and molecular cloning of the mRNA for the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
MEDLINE=83182019; PubMed-6820340;
Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
Discounse construction, identification, and DNA sequence.";
DNA 1:335-343(1982).
                                                                                                                                                                                    55.7%; Score 1033.5; DB 2; Length 571;
.larity 61.9%; Pred. No. 3.2e-71;
Conservative 41; Mismatches 72; Indels 13;
                                          Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T. Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai Sugano S.,
                                                                                                        "NEDO human cDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK130825; BAC85440.1;
                                                                                                                                                       62602 MW; E920D06277B8D2FF CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
gessilon chain C region.
Rattus norvegicus (Rat).
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MEDLINE=83064537; PubMed=6292865;
Hellman L., Pettersson U., Engstro
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                                TISSUE=Thymus;
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191 AHTRRCPDHEPRGVITYLIPPSPLDLYQNGAPKLICLVVDLESEK-NVNVTWNQEKKISV 249
                                                                           SASQWYTKHHNNATTSITSILPVVAKDWIEGYGYQCIVDHPDFPKPIVKSITKTPGQRSA 309
                                                                                                                                           Potential.
Interchain (with light chain) (Probable).
By similarity.
By similarity.
                                                                                                                          PEVYMLPPSPEETGTTRIVTCLIRGFYPSEISVQWLFNNBEDHTGHHTTTRPQKDHGTDP
                                                      NHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mu-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bernstein K.E., Alexander C.B., Reddy E.P., Mage R.G.;
"Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain
of VHAZ allotype: comparisons with VHa1 and membrane mu sequences.";
J. Immunol. 132:496-495[1984].
                                                                                                                                                                                                                                                                                                                                P04221.

20-MR-1991 (Rel. 04, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11g mu chain C region membrane-bound form.
Oryctolagus cuniculus (Rabbia) (Rabbia) (Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
Comment=During differentiation, B lymphocytes switch from
expression of isoform Membrane-bound to isoform Secreted;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Immunoglobulin C region;
                                                                                                                                                                                                                297 SFFLYSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
                                                                                                                                                                                                                                                                                                                   479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Membrane-bound;
IsoId=P04221-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P03988-1; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=84088930; PubMed=6418803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (A2 ALLOTYPE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEGM, PP00047; ig; 4. SWART; SW0407; ig; 4. PROSITE; PS50815; IG_LIKE; 4. PROSITE; PS00290; IG_MIC; 3. Alternative splicing; Glycopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; K01357; AAA31293.1; -.
                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain;
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DOMAIN 107 222
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HSSP; P01861; 1ADQ.
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2223
328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
                                                                                                                                                                                                                             MEDLINE=83117774; PubMed=6818553;
Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
"Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 HVTWLVDGQEAENLFPYTTRPKREGGQTFSLQSEVNITQGQMMSSNTYTCHVKHNGSIFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FHHHHHHTLSLPES-----GPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKV
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 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=84236092; PubMed=6329728;
MEDLINE=84236092; PubMed=6329728;
MEDLINE=84236092; PubMed=6329728;

The nucleotide sequence of the mouse immunoglobulin epsilon gene:
comparison with the human epsilon gene sequence.";
EMBO J. 1:1117-1123(1982).
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R PIR; A02144; EHMS.

R PIS; A02144; EHMS.

R HSSP; P01854; IFPS.

R INCEPPO; IPR007110; Ig-like.

R INCEPPO; IPR003006; Ig_MHC.

R PEm; PF00047; ig; 4.

R RNART; SM00407; IGC1; 2.

R RNART; SM00407; IGC1; 2.

R RNART; SM00200; IG_MHC.

R PROSITE; PS50835; IG_LIKE; 4.

R PROSITE; PS00290; IG_MHC, 3.

R QIYCOPTOCLEIN; Immunoglobulin C region; Immunoglobulin domain.
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1.3e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53; Mismatches 130; Indels
                                                                                                                                                             Honjo T.; Submitted (APR-1986) to the EMBL/GenBank/DDBJ databases.
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(GlcNAc...)
(GlcNAc...)
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44.8%; Pred. No. 1
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Best Local Similarity 44.8
Matches 155; Conservative
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DILMISRIPEVICAVADASHEDPEVOENWYVDGMEVHNAKIKPREEOFNSTFRAVSVLIV 325
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                                                                                                                                                                                                                      326 VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCL
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                                                                                                                                                                                         RGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPKREGGQTFSLQSE
                                                                                                                                                                                                                                                                                                                       VIVISSNF-GIQIYICNVDHKPShIKVDKIVERKCCVECPPCPAPPVAGPSVFLFPPKPK
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Homo.
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TISSUB=Human rectum tumor;

Bloecker H., Beccher M., Wees H.W., Weil B., Amid C., Osanger Bloecker H., Weemann S.;

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, SA640814; CAEA5331.1;

Hypothetical protein.

SEQUENCE 464 AA; S1099 WW; 2FCA72C66E8A0ABC CRC64;
                                                                                                 Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.8%; Score 496.5; DB 2; Length 36.5%; Pred. No. 6.2e-30; ive 58; Mismatches 118; Indels
                                                                                                                                             Indels
                               il protein.
464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothelical protein DKFZp686C15213.
                                                                                            26.8%; Score 496.5; DB 2; 36.5%; Pred, No. 6.2e-30; ive 58; Mismatches 118;
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                                                                                                                  Best Local Similarity 36.58
Matches 118; Conservative
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Matches 118; Conservative
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02-MAR-2004 (
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                               Hypothetical
SEQUENCE 46
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         PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : | | | | : : | | | : | | | HINSINDLRVSFPVDSELPPNVSVF---IPPRDSFSGGTRKSRLICQATGFSPKQISVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 WLRDGÓKVESGVLTKPVEAETKGAGPATFSISSMLTITESDWLSQSLYTCRVDHRGIFFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 KNVSMSSECSTTPSPGIQVFPIAPSFADTFLSKSARLICLVTDLT-TYGSLNISWASHNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 RLA---PEVYMLPPSPEE--TGTTRIVICLIRGFYPSEISVQWLFNNEEDHTGHHTTTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WLVDGQEAEN---LFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFE
                                                                                                                                                                                                                                                                                                                                                                        5 HHHHTLSLPESGPV-TIIPPTVKLFHSSCDPR----GDAHSTIQLLCLVSGFSPAKVHVT
       (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKDHGTDPSFFLYSRMLVNKSIWEKGNLVTCRVVHEALP---GSRTLEKSLHYSAG 341
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                                                   (Probable)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                        (Potential).
(Potential).
(Potential).
(Potential).
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Interchain (with heavy chain) (P By similarity.

By similarity.

By similarity.

N-linked (GlONAc. .) (Potentia N-linked (GLONAc. .) (Potentia N-linked (GLONAc. .) (Potentia N-linked (GLONAc. .) (Potentia N-linked (GLONAc. .) (Potentia N-linked (GLONAc. .) (Potentia N-linked (GLONAc. .) (Potentia N-linked (GLONAc. .) (Potentia N-linked (GLONAc. .) (Potentia N-linked (GLONAc. .) (Potentia
                                                                                                                                                                                                                                                                              26.8%; Score 497.5; DB 1; Length 479;
.larity 32.9%; Pred. No. 5.4e-30;
Conservative 61; Mismatches 153; Indels 25
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THE GERMAN HUMAN CDNA CONSORTIUM;
THE GERMAN HUMAN CDNA CONSORTIUM;
THE GERMAN HUMAN CDNA CONSORTIUM;
THE GERMAN HUMAN CDNA CONSORTIUM;
TODO G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
THERL; MACA 68041; CAR45931.1;
InterPro; IPRO031010; Ig-like.
TINTERPRO; IPRO031010; Ig-like.
TINTERPRO; IPRO031010; Ig-like.
TINTERPRO; IPRO030599; Ig-MHC.
TINTERPRO; IPRO030506; Ig-MHC.
TINTERPRO; IPRO03506; Ig-MHC.
THERPRO; IPRO03506; Ig-MHC.
THERPRO; IPRO03506; Ig-MHC.
THERPRO; IPRO03506; Ig-MHC.
                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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05-JUL-2004 (TYEMBLrel. 27, Created)
05-JUL-2004 (TYEMBLrel. 27, Last second-2010-2004 (TYEMBLrel. 27, Last ann Hypothetical protein DKFZp686C15213.
Name=DKFZp686C15213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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Pfam; PF07654; Cl.set; 3
Pfam; PF00047; ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00406; IGc; 3.
PROSITE; PS50835; IG LIKE
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479 AA;
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nes 117; Conserv
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DISULFID
CARBOHYD
CARBOHYD
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CARBOHYD
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58 VTW----LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNITQGQMMSSNTYTCHVKH--- 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 KAVSMSSECSTTPSPGIQVFPIAPSFADTFLSKSARLICLVTDLT-TYGSLNISWASHNG
                                                                                                                                                                                                                                                                                                                                                              60 WLVDGQEAEN---LFPYTTRPKREGGQTFSLQSEVNITQGGWMSSNTYTCHVKHNGSIFE
                                                                                                                                                                                                                                                                                                                                                                                                    151 WLRDGQKVESGVLTKPVEAETKGAGPATFSISSMLTITESDWLSQSLYTCRVDHRGIFFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 KALDIHMNITESHPNATFSAMGEASVCAEDWESGEQFTCTVTHADLPFPLKHTISK--SR
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                                                                                                                                                                                                                                                                                                                   HSNSNRDLRVSFPVDSELPPNVSVP---IPPRDSFSGSGTRKSRLICOATGFSPKQISVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 DS---SRKCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGK
                                                                                                                                                                                                                                                                             HHHHTLSLPESGPV-TIIPPTVKLFHSSCDPR----GDAHSTIQLLCLVSGFSPAKVHVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ27104 fis, clone SPL04981, highly similar to 1g gamma-2 chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFHHHHHHTLSLPESGPVTIIPPTVK---LFHSSCDPRGDAHSTIQLLCLVSGFSPAKVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

TISSUE=Spleen;

Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,

Ranehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,

Fanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,

Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,

Sugiyama T., Irie R., Osogi T., Sato H., Nishikawa T., Sugiyama A.,

Kawakami B., Nagai K., Isogai T., Sato H., Nishikawa T., Sugiyama A.,

"NEDO human DDNA sequencing project.",

Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AK130614; BAC85395.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
                      (Potential). (Potential). (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 OKDHGIDPSFFLYSRMLVNKSIWEKGNLVTCRVVHEALP---GSRTLEKS
                                                                                                                                                                                        ; Score 495.5; DB 1; Length
; Pred. No. 7.3e-30;
61; Mismatches 148; Indels
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    46
1114
2112
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445
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114,
212,
261
277
284
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                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 116; Conserv
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BAC85395;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
  SHOPMINGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYLLPPSREEMTKNQVSLTCL 385
                                                                                                           441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (A2 ALLOTYPE).

MEDLINE=84088930; PubMed=6418803;

Bernstein K.E., Alexander C.B., Reddy E.P., Mage R.G.;

"Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain of VHa2 allotype: comparisons with VHa1 and membrane mu sequences.";

J. Immunol. 132.490-495 (1984).

-! SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                            (Probable).
                                                                   IRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKSIWEKGNLVT
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CH2.
CH3.
CH4.
Interchain (with light chain) (Probable)
                                                                                                                                                                                                                                                                                                                                         23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10 mu chain C region secreted form.
Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing, Named isoforms=2, Comment=During differentiation, B lymphocytes switch from expression of isoform Membrane-bound to isoform Secreted;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By similarity.
By similarity.
Interchain (with heavy chain) (PBy similarity.
Interchain (with heavy chain) (PBy similarity.
                                                                                                                                                                                                                                                                                                      458 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P04221-1; Sequence=External;
                                                                                                                                                                            | |:|||| | :||| | CSVMHEALHNHYT-QKSLSLSPG 463
                                                                                                                                                      CRVVHEALPGSRTLEKSLHYSAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; K01357; -; NOT_ANNOTATED_CDS.
PIR; A02164; MHRB.
INSSP: P01861; 120.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003506; Ig_MHC.
                                                                                                                                                                                                                                                                                                      STANDARD;
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NGSIFEDSSRKCADSNP-----RGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKG 162
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Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
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EMBL; AK131045; BAC85483.1;
SEQUENCE 468 AA; 51715 MW; CB3A94413B6C36CA CRC64;
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02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ29011 fis, clone DMC03382, highly similar to Ig
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MEDLINE=22388257; PubMed=12477932;

A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Lausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Lausher R.D., Colline F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

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B And S.S., Loquelland N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

B Raha S.S., Loquelland N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

B Raka S.S., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

R Richards S., Wolly K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

R Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
Rubit BC062335, AAH62335.1;
Rubit BC062335, AAH62335.1;
Rubit BC062335, RAH62335.1;
RuterPro; IPR001599; IG-1ike.
RuterPro; IPR001599; IG-1ike.
RuterPro; IPR003050; IG-MHC.
RuterPro; IPR003050; IG-MHC.
RuterPro; IPR003050; IG-MHC.
RuterPro; IPR003059; IG-NHC.
RuterPro; IPR003059; IG-NHC.
RuterPro; IPR00409; IG-NHC.
Ruser; SM00409; IG-1 3.
Ruser; SM00409; IG-1 3.
Ruser; SM00409; IG-1 3.
Ruser; SM00409; IG-NHC; UNKNOWN_2.
Ruser; PR00290; IG-MHC; UNKNOWN_2.
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Pred. No. 2.6e-29;
L; Mismatches 130;
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26.3%; Soc
Best Local Similarity 35.0%; Prv
Matches 124; Conservative 61;
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PRELIMINARY;
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SEQUENCE FROM N.A.
TISSUE=Spleen;
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SEQUENCE OF 2-326 FROM N.A.
MEDLINE=82197621; PubMed=6804948;
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P01859;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
KIDLINE=22388257; FubbMed=12477932;
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Staplecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Wolfer Y., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muray D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whilting M.M., Madan A., Young A.C., Shevohenko Y., Boutfard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Arzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Andones S.J., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length human
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                                                          YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTIS 355
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                                                                                                                                                               SRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTT
                                                                                                                            KLPGKRLAPEVYMLPPSPEB-TGTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTR
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                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC062335; AAH62335.1; --
Hypothetical protein.
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465 AA; 51325 MW; FDDB9348ADC37E6D CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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AAH62335;
02-MAR-2004 (TrEMBLrel.
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AAH62335
AAH62335
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"Linkage and sequence homology of two human immunoglobulin gamma heavy
chain constant region genes.";
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                                                                            169 SRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTT
                                                                                                                                                                                                                              KLPGKRLAPEVYMLPPSPEE-TGTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTR
                                                                                                                                                                                                                                                                                                                                                                                    POKDHGTDPSFFLYSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                     414 PMLD - SDGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT - QKSLSLSPG 464
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Can. J. Biochem. 57:758-767(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=83001943; PubMed=6811139;
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"Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
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MEDLINE-80114419; PubMed=118920;
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M. note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains.";
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"The primary structure of a human IgG2 heavy chain: genetic,
evolutionary, and functional implications.";
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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MEDLINE=81007873; Pubmed=6774012;
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S -> A (in myeloma proteins TIL and ZIE).

FyrIad-vAR 003899.

C -> S (in Ref. 3).

Fyriad-vAR CG878CF9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                       WEDLINE=72033500; PubMed=4940472;
Milstein C., Frangione B.;
"Disulphide bridges of the heavy chain of human immunoglobulin G2.";
Biochem. J. 121:217-228 (1971).
                                                                                                                                                       Sequence Or 1-121 (DOT)
MEDULINE-9525598; Pubmed-7737190;
Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri
"Characterization of the two unique human anti-flavin monoclonal
immunoglobulins.";
Eur. J. Biochem. 228:886-893(1995).
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.larity 36.2%; Pred. No. 2.4e-29;
Conservative 57; Mismatches 120; Indels 29
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GO; GO: 0005624; C: membrane fraction; NAS.
GO; GO: 0005625; F: antigen binding; TAS.
GO; GO: 0005955; P: antigen binding; TAS.
GO; GO: 0005955; P: mumue response; NAS.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig. MHC.
Pfam; PF00147; Ig.cl.
InterPro; PF00290; Ig. MHC.
InterPro; PF00290; Ig. MHC.
InterPro; Ig.cl.
InterPro; Ig.cl.
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Franctione B., Milstein C., Pink J.R.L.;
Structural studies of immunoglobulin G.";
Nature 221:145-148(1969).
                        REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank.
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HSSP, P01857, 10QX.
Genew, HGNC:5526, IGHG2.
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MEDLINE=95255298; PubMe
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69 VIVPSSNF-GIQIYICUVDHKPSNIKVDKIVERKCCVECPPCPAPPVAGPSVFLFPPKPK
                                                                                                                                                                                                                                                                                                                                      [1] SEQUENCE FROM N.A.
[2] TISSUE-Human esophagus tumor;
[3] TISSUE-Human esophagus tumor;
[4] TISSUE-Human esophagus tumor;
[5] THE GERMAN HUMAN CDNA CONSORTIUM;
[5] Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
[6] Ambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
[7] Manbutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
[8] Submitted (Aug-2003) to the EMBL/GenBank/DDBJ databases.
[8] State Decoration of the EMBL/GenBank/DDBJ databases.
[8] STAGE-FOOT IPRO0159 1 gg.1.
[8] InterPro; IPRO01596; Ig_MHC.
[9] InterPro; IPRO01596; Ig_MHC.
[9] InterPro; IPRO01596; Ig_MHC.
[9] Fean; PRO047; ig; 3.
[9] SMART; SMO0406; IGV; 1.
[9] SMART; SMO0406; IGV; 1.
[9] PROSITE; PSSO835; IG_LIKE; 3.
[9] PROSITE; PSSO835; IG_LIKE; 3.
[9] PROSITE; PSSO835; IG_LIKE; 3.
[9] PROSITE; PSSO835; IG_LIKE; 3.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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05-0TL-2004 (TrEMBLrel. 27, Last sequence update)
05-0TL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686104196 (Fragment).
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26.2%; Score 486.5; DB 2;
Best Local Similarity 36.2%; Pred. No. 3.2e-29;
Matches 117; Conservative 57; Mismatches 120;
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Best Local Similarity Matches 117; Conserv

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141 D-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPV 199
                      219 DTLMISRIPEVICCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTV 278
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
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Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
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26.2%; Score 486.5; DB 2; Length 417;
Best Local Similarity 36.2%; Pred. No. 3.2e-29;
Matches 117; Conservative 57; Mismatches 120; Indels 29
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02-MAR-2004 (TYEMBLrel. 27, Last sequence update)
02-MAR-2004 (TYEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686I04196 (Fragment)
DKFZP686I04196.
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Minimum DB e Maximum DB e

Searched:

Database :

Abp96591 Brushtail Aao19668 GE2 fusio Abp96584 Duckbille Aao19667 Human IgE Aau80288 Human IgE Aau80288 Human IgE Aau80289 Human IgE Aar83559 Fo (epsilo Aar77221 Human IgE Aar77241 Human IgE Aar77241 Human IgE Aar77241 Human IgE Aar77241 Human IgE Aar77241 Human IgE Aar77241 Human IgE Aar77241 Human IgE Aar77241 Human IgE Aar77241 Human IgE Aar8666 Human IgE Aar80291 Interleuk Aau80291 Interleuk Aao19666 Human IgE Aam80240 Human IgE Aam80240 Human IgE Aam80240 Human IgE Aam80240 Human IgE Aam80240 Human IgE	ABNTS				ossum CH2, human CH3 and opossum CH4.	3; vaccination; infection; allergy;									preventing the harmful effects of		ic peptide consisting of the heavy e opossum IgE and the heavy chain was shown to cause a stronger an peptides consisting of the same peptides, particularly those constant regions, can be used for rial and viral infections and en and food allergies and eczema.
ABP96591 AAO19668 AAD96584 AAO19666 AAU80285 AAU80285 AAU80285 AAR83529 AAR77241 AAR77241 AAR77241 AAR77241 AAR77243 AAU80293 AAU80291 AAD90291 AAD90291 AAD90291	ALIGNMENT	342 AA.			ing of opoi	in E; IgE, peptide.									ful for	lish.	unogen of th dan It nase th cogenic chain bacte poll
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266 276 276 276 276 276 276 276 276 276		: 1 205 AAB06205 s	AAB06205;	.2-SEP-200 :2-NOV-200	mmunogeni	Human; opos asthma; ecz	oidelphis Iomo sapie Chimeric.	1020002572	1-MAY-200	1-0CT-199	2-NOV-199	(RESI-) RES	Hellman LT;	PI; 2000-	mmunogeni mmunoglob	Disclosure;	he present hain const constant re colyclonal egions fro egions fro accination (llergies, Updated or
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1759

Result No.

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ORORO pro Immunogen

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Gaps

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host, e.g. CHO, cells. The invention provides methods and materials related to expressing chimeric IgE proteins. Nucleic acid vectors, host cells, and methods for producing chimeric IgE polypeptides are provided. When administered to a mammal, the chimeric polypeptides can reduce the IgE antibody effects of IgE-related diseases such as asthma, allergies
                                                                                                                                                                                                                                                                                                                                                                           243 BETGTTRIVTCLIRGEYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLV
                                                                                                                                                                                                                                         TISTPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAE
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                                                                                                                                                                                                                                                                                         69 NLFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRKCADSNPR
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                                                                                                                                                   Score 1786; DB 8;
Pred. No. 3.6e-140;
0; Mismatches 0;
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                                                                                                                             EFHHHHHHTLSLPESGPVTIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGPSPAKVHVTW
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                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New host cell comprising a nucleic acid vector comprising a cytomegalovirus promoter, an Ig leader sequence, an insert sequence 5040 late polyadenylation sequence, useful in producing a chimeric polypeptide.
                                                                        0;
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                                        100.0%; Score 1856; DB 3; 100.0%; Pred. No. 5.4e-146;
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                                                                        Mismatches
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N-PSDB; ADF90024, ADF90023.
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The present invention relates to a composition comprising a polypeptide and an aluminum compound, where the polypeptide comprises a self-tog polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide. ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, ADN0661, 
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antiasthmatic; dermatological.
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Pred. No. 3.6e-140;
); Mismatches 0;
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Best Local Similarity 99.4
Matches 334; Conservative
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Homo sapiens.
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The present sequence is the protein sequence of an opossum CH2-human CH3-opossum CH4 chimeric IgE polypeptide including a C-terminal polyhistidine sequence (OSO-H). A vector comprising DNA encoding OSO-H can be used for recombinant production this chimeric IgE in host, e.g. CHO, cells. The invention provides methods and materials related to expressing chimeric IgE proteins. Nucleic acid vectors, host cells, and methods for producing chimeric IgE polypeptides are provided. When administered to a mammal, the chimeric polypeptides can reduce the IgE antibody effects of IgE-related diseases such as asthma, allergies and eczema.
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                                                    New host cell comprising a nucleic acid vector comprising a cytomegalovirus promoter, an Ig leader sequence, an insert sequence or SV40 late polyadenylation sequence, useful in producing a chimeric IgE polypeptide.
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Pred. No. 3.7e-140;
); Mismatches 0;
                                                                                                                                                                                                      Claim 3; SEQ ID NO 14; 23pp; English.
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Best Local Similarity 99.4%;
Matches 334; Conservative
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N-PSDB; ADF90032.
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The present sequence is the protein sequence of an opossum CH2-human CH3-opossum CH4-chimeric IgE polypeptide (modOSOSO). The coding sequence for modOSOSO contains point mutations in the human CH3 domains that abolish mast cell receptor binding. A vector comprising DNA encoding modOSOSO can be used for the recombinant production of the materials IgE in Nost, e.g. CHO, cells. The invention provides methods and materials related to expressing chimeric IgE proteins. Nucleic acid vectors, host cells, and methods for producing chimeric IgE polypeptides can reduce the IgE antibody effects of IgE-related diseases such as asthma, allergies and eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New host cell comprising a nucleic acid vector comprising a cytomegalovirus promoter, an Ig leader sequence or SV40 late polyadenylation sequence, useful in producing a chimeric IgE
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                                                                                                                                                                                                                                                                                                                                Fuentes A, Magnusson A;
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WO2003096966-A2
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                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a composition comprising a polypeptide and an aluminum compound, where the polypeptide comprises a self-igh polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide. ADN00643, ADN00644, ADN00654, ADN00654, ADN00654, ADN00656, ADN00656, ADN00658, ADN00658, ADN00651, ADN00651, ADN00659, ADN00659, ADN00659 or level of detectable free IgE in the mammal. The composition is useful for inducing an anti self-ige antibody response in a mammal for treating or preventing allergies. The present sequence is an OSO protein, used to illustrate the invention. The OSO-H protein contains an opossum CH2 IgE domain followed by a human CH3 IgB domain followed by a nopossum CH4 IgE domain. The OSO-H protein also contains a C-terminal polyhistidine tag.
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                                                                                                                                                                                      New composition comprising a self-igE polypeptide and an aluminum compound, useful for inducing an anti self-igE antibody response in mammal for treating or preventing allergies.
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                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 16; 102pp; English.
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Matches 334; Conservative
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Didelphis virginiana.
Homo sapiens.
                                      Persson
                                                                                                      2004-248376/23
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                                      Hellman LT,
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ADN00656 standard; protein;

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The present sequence is the protein sequence of an opossum CH2-human CH3-opossum CH2-human CH3-opossum CH4 (OSOSO) chimeric IgE polypeptide. A vector comprising DNA encoding OSOSO can be used for recombinant production of the chimeric IgE in host, e.g. CHO, cells. The invention provides methods and materials related to expressing chimeric IgE proteins. Nucleic acid vectors, host cells, and methods for producing chimeric IgE polypeptides are provided. When administered to a mammal, the chimeric polypeptides can reduce the IgE antibody effects of IgE-related diseases such as asthma, allergies and eczema.
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                   opossum; human; vaccine; antiallergic;
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Pred. No. 9.9e-139;
; Mismatches 3;
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                IgE; immunoglobulin; antibody;
antiasthmatic; dermatological.
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Homo sapiens.
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The present invention relates to a composition comprising a polypeptide and an aluminium compound, where the polypeptide comprises a self-1gE polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide:
ADNOG643, ADNOG644, ADNOG654, ADNOG664, ADNOG664, ADNOG6644, A
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                                                                                                                                                                                                                  Antiallergic; Vaccine; self-IgE; ORO; OSO; allergy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gansson A;
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es 328; Conservative
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                                                                                                                                                             OSOSO protein, SEQ ID
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RESULT 8 ADN00656

310 IWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342

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The present sequence is the protein sequence of an opossum CH2-human CH3-opossum CH3-buman CH3-opossum CH4 chimeric IgE polypeptide including a C-terminal polyhistidine sequence (modoSoSo-H). The coding sequence for modoSoSo-H contains point mutations in the human CH3 domains that abolish mast cell receptor binding. A vector comprising DNA encoding modoSoSo-H combinant production of the chimeric IgE in host, e.g. CHO, cells. The invention provides methods and materials related to expressing chimeric IgE proteins. Nucleic acid vectors, host cells, and methods for producing chimeric IgE polypeptides are provided. When administered to a mammal, the chimeric polypeptides can reduce the IgE antibody effects of IgE-related diseases such as asthma, allergies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 IDIPESGPUTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAEN 284
105 TLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTASPGKRLAPEVYMLPPSPEET 464
                                                                    10 LSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAEN
                                           GTTRIVICLIRGEYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKS
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                                                                                                                                310 IWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
                                                                                                                                                          Opossum-human chimeric IgE polypeptide.
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Best Local Similarity 98.5
Matches 328; Conservative
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Didelphis virginiana
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Larity 98.5%; Pred. No. 9.9e-139;
Conservative 2; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                               Antiallergic, Vaccine, self-IgE; ORO; OSO; allergy.
    Gansson A;
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                                                                                                                                       ADN00652 standard; protein; 557
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328; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New host cell comprising a nucleic acid vector comprising a cytomegalovirus promoter, an Ig leader sequence, an insert sequence or SV40 late polyadenylation sequence, useful in producing a chimeric IgE polypeptide.
                        LFPYTTRPKREGGGTFSLQSEVNITQGQWMSSNIYTCHVKHNGSIFEDSSRKCADSNPRG
                                                                                        345 VSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNG
                                                                                                                                                                                                                       GTTRIVICLIRGEYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKS
LPPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG
                                                               130 VSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNG
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                                                                                                                                                                                                GITRIVICLIRGFYPSEISVQWLFNNEEDHIGHHTITRPQKDHGIDPSFFLYSRMLVNKS
                                                                                                                               TLIVISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTIKLPGKRLAPEVYMLPPSPEET
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                                                                                                                                                                                                                                                                310 IWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
                                                                                                                                                                                                                                                                                           IWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Opossum-human chimeric IgE polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                   ADF90037 standard; protein; 566
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Didelphis virginiana.
Homo sapiens.
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N-PSDB; ADF90036.
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                                                                                                         LSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAEN
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Length 566;
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Score 1772; DB 8;
Pred. No. 1e-138;
2; Mismatches
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95.5%;
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Best Local Simi
Matches 328;
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illustrate the invention. The OSOSO protein contains an opossum CH2 IgE domain followed by an opossum CH3 IgE domain followed by an opossum CH3 IgE domain followed by an opossum CH3 IgE domain followed by an opossum CH4 IgE domain. The OSOSO-H protein also contains a C-terminal polyhistidine tag.
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                                                                                                                       225 IDIPESGPVTIIPPTVKLFHSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAEN
                                                                                                                                                                                           VSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNG
                                                                                                                                                   LFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG
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                                                                     Length 566;
                                                                    Score 1772; DB 8; Length 5
Pred. No. 1e-138;
2; Mismatches 3; Indels
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                                                                    Query Match
Best Local Similarity 98.5%;
Matches 328; Conservative
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N-PSDB; ADN00649.
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polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide: ADN00643, ADN00656, ADN00656, ADN00658, ADN00651). Administration of the composition to a mammal reduces the level of detectable free IgE in the mammal. The composition is useful for inducing an anti self-IgE antibody response in a mammal for treating or preventing allegiles. The present sequence is an OSO procein, used to illustrate the invention. The medoSOSO-H protein contains an opossum CH2 IGE domain followed by a human CH3 IGE domain followed by an opossum CH2 IGE domain. The andOSOSO-H protein also contains point mutations in the human CH3 ide domain followed by an opossum CH4 IGE domain. The andOSOSO-H protein also contains point mutations in the terminal polyhistidine tag.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GITRIVICLIRGEYPSEISVQWLFNNBEDHIGHHITIRPQKDHGIDPSFFLYSRMLVNKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRKCADSNPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRMLVNKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLIVISTLPVGTRDWIBGETYQCRVTHPHLPRALMRSTTASPGKRLAPEVYMLPPSPEET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.5%; Score 1772; DB 8; Length 566; ilarity 98.5%; Pred. No. 1e-138; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antiallergic; Vaccine; self-IgE; ORO; OSO; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1e-138;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H-OCO-H protein, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s,
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N-PSDB; ADN00660.
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                                                                              The present invention relates to a composition comprising a polypeptide and an aluminium compound, where the polypeptide comprises a self-IgE polypeptide sequence (e.g. an ORO polypeptide comprises a self-IgE ADM06643, ADM06643, ADM06654, ADM06654, ADM06656, ADM06656, ADM06656, ADM06656, ADM06656, ADM06656, ADM06656, ADM06659 or ADM0661). Administration of the composition to a mammal reduces the invent of detectable free IgE in the mammal. The composition is useful for preventing allergies. The present sequence is H-OCO-H protein, used to preventing allergies. The H-OCO-H protein contains an opossum CH2 IgE domain. The H-OCO-H protein contains an opossum CH2 IgE domain. The H-OCO-H protein also contains a N- and C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                            120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.
New composition comprising a self-IgE polypeptide and an aluminum compound, useful for inducing an anti self-IgE antibody response in a mammal for treating or preventing allergies.
                                                                                                                                                                                                                                                                                                                                                                                                           LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGKKQRNGTLTVTSILPVVTQDMIEGETYQCRVTHPHLPRALVRSMTKLASPGKRLAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 VYMLPPSPEETGTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSF
                                                                                                                                                                                                                                                                                                                                                    1 BPHHHHHHLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW
                                                                                                                                                                                                                                                                                                                                                                             1 BEHHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW
                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 RKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKL - - PGKRLAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VYMLPPSPEETGTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSF
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccination; infection; allergy;
                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                             Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLYSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLYSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 344
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                              DB 8;
                                                                                                                                                                                                                                                                                             Score 1759; DB 8;
Pred. No. 6.7e-138;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dog; opossum; immunoglobulin E; IgE; asthma; eczema; immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB06208 standard; protein; 341
                                                        Claim 3; Fig 23; 102pp; English
                                                                                                                                                                                                                                                                                              94.8%;
95.3%;
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(first entry)
                                                                                                                                                                                                                                                                                                          Best Local Similarity 95.3
Matches 328, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Didelphis virginiana
                                                                                                                                                                                                                                                                    Sequence 353 AA;
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22-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                            The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant regions 1 from the dog. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIOLLCLVSGFSPAKVHVTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVDGQEAENLFPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLPPSPEETGTTRTVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EFHHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KCADSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                            Immunogenic polypeptides useful for preventing the harmful effects immunoglobulin \boldsymbol{E} in mammals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.6%; Score 1644.5; DB 3;
88.0%; Pred. No. 2.2e-128;
tive 17; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              completed: November 14, 2004, 14:58:12
                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 2; 50pp; English
98US-0106652P.
99US-00401636.
                                                                              (RESI-) RESISTENTIA PHARM AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 301; Conservative
                                                                                                                                                                               WPI; 2000-365342/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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02-NOV-1998;
22-SEP-1999;
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TR-03-401-030-0108601101

F007 01.17.61

November 14, 2004, 15:03:41; Search time 24 Seconds (without alignments) 945.032 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-401-636-8 1856 I EPHIHHHHTLSLPESGPVTI......HEALPGSRTLEKSLHYSAGN 342

Title: Perfect score: Sequence:

Scoring table:

478139 seqs, 66318000 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

417130 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 342

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

lssued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	equence 56, equence 1, equence 1, equence 1, equence 1, equence 1, equence 1,	equence 17, equence 17, equence 17, equence 17, equence 17, equence 17, equence 6,	Sequence 6, Appli Sequence 12, Appli Sequence 9, Appli Sequence 9, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 27, Appli Sequence 27, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 36, Appli Sequence 36, Appli Sequence 36, Appli Sequence 36, Appli Sequence 36, Appli	יה פסוונים לי
QI	32-539D- 66-163B- 02-096-1 02-077-1	-08-646-981- -08-4646-981- -08-466-981- -08-466-151- -08-436-463-	US-08-03-3-6 US-08-761-277A-47 US-08-55-586-9 US-08-55-586-9 US-09-301-593-22 US-08-579-940-8 US-08-579-940-7 US-09-579-940-7 US-09-579-940-7 US-09-968-362A-27 US-09-968-362A-28 US-09-968-362A-28 US-09-483-588-5 US-09-483-588-5 US-09-483-588-5 US-09-483-588-5 US-09-483-588-5 US-09-483-588-5	
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Result No.	ተሪያ ማ 4 የ	1008701	111111111111111111111111111111111111111	

Sequence 3, Appli	Sequence 3, Appli	٦,	Sequence 1, Appli	Ŋ	'n	Sequence 7, Appli	m	ø	H	Ä	1066	σ,		ď	106	10, App	4, 4
US-08-808-720-3	US-09-467-638-3	US-08-808-720-1	US-09-467-638-1	US-08-808-720-5	US-09-467-638-5	US-09-883-777-7	US-09-483-588-3	US-09-483-588-6	US-09-428-082B-12	US-09-428-082B-10	US-09-428-082B-1066	US-09-883-777-9	US-09-178-869-2	US-09-761-413-2	US-09-428-082B-1062	US-09-854-864-10	US-09-483-588-4
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326	326	328	328	331	331	309	218	218	247	569	252	300	331	331	248	281	218
22.0	22.0	22.0	22.0	22.0	22.0	21.9	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.7	21.7	21.7
407.5	407.5	407.5	407.5	407.5	407.5	406	405.5	404.5	404.5	404.5	404	404	404	404	403.5	403	402.5
28	29	30	31	32	33	34	35	36	37		გ	40	41	42	43	44	45

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	Length 113; Indels
di sk	DB 2.3e-4
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539D NA NA P. P. P. P. P. P. P. P. P. P. P. P. P.	Score Pred. 0; Mi
T 1  -232-539D-56  ent No. 5965709  subrad INFORMATION: APPLICANT: Presta, Leonard G. APPLICANT: Presta, Leonard G. APPLICANT: Presta, Leonard G. APPLICANT: Jardieu, Paula M. ITILE OF INVENTION: ADDRESSEE: Genettech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA STATE: California COMPUTER: READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb COMPUTER: TEM PC compatible COMPUTER: TEM PC compatible COMPUTER: TEM PC compatible COMPUTER: 1 DNA Way CITY: South San Francisco STATE: California COMPUTER: 1 DNA Way CITY: South San Francisco CUNTRY: USA STATE: California COMPUTER: 1 DNA Way CITY: South San Francisco CUNTRY: Win PAIN BC COMPATIBLE COMPUTER: 1 DNA Way CITY SANDIL CATION DATA: APPLICATION NUMBER: 08/17868 FILING DATE: 07-0N-1994 ARDELCATION NUMBER: 09/174768 FILING DATE: 07-0N-1994 ARDELCATION NUMBER: 09/174768 FILING DATE: 14-AUG-1991 ARDELCATION NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER: 39,044 REFERENCE JOCKT NUMBER:	31.2%; 98.2%; ive
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T 1  -232-539D-56  cut No. 5965709  where 56, Application  APPLICANT: Presta,  APPLICANT: Presta,  APPLICANT: Presta,  APPLICANT: Presta,  APPLICANT: Presta,  APPLICANT: Presta,  CORRESPONDENCE ADDRESSEE:  GALIECTIS GALICATION:  STATE: California  COUNTRY: USA  STATE: California  CONFUTER READABLE FO  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IBM PC  COMPUTER: IMDRESTA  PREDICATION UNMERR  PLILING DATE: 14-A  APPLICATION ON A  REPERENCE/DOCKET N  TELEPHONE: SCOOLOGY: LINEAR  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH: 113 and no  LENGTH:	Έ
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124 DSNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKE 183
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FACENTERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended):
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended):
TITLE OF INVENTION: MORPER: US/09/802,077
CURRENT APPLICATION NUMBER: US 08/405,617
FRIDR PILING DATE: 1995-03-15
FRIDR PILING DATE: 1994-01-26
FRIDR PILING DATE: 1994-01-26
FRIDR PILING DATE: 1994-01-26
FRIDR PILING DATE: 1994-01-26
FRIDR PILING DATE: 1994-08-14
FRIDR PILING DATE: 1991-08-14
FRIDR FILING DATE: 1991-08-14
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Pred. No. 1.1e-45;
0; Mismatches 2; Indels 1
                                                         Length 109;
                               Score 548.5; DB 4; Dels.
Pred. No. 1.18-45;
2; Indels
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APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: IGE Antagonists
NUMBER OF SECHENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genenech, Inc.
STRES: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTY: USA
ZIP: 94080
COMPUTER READABLE FORM:
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, Sequence 54, Application US/08232539D

; Patent No. 5965709

; GENERAL INFORMATION:
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Best Local Similarity 97.2%;
Matches 106; Conservative
                                                         Query Match
Best Local Similarity 97.23
Matches 106; Conservative
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ORGANISM: Homo sapiens
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   US-09-802-096-1
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Sequence 1, Application US/09802096;
Sequence 1, Application US/09802096;
Settent No. 668533
GENERAL INFORMATION:
APPLICANT: Jardieu, Penard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended TITLE OF INVENTION: MUMBER: US/09/802,096
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/105,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR PILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-14
PRIOR FILING DATE: 1992-06-07
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
NUMBER OF SEQ ID NOS: 64
SEQ ID NOS: 64
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182 KEEKORNGTLIVISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTIKLPG 232
                                                                                                                         61 KEEKQRNGTLIVISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTIKTSG 111
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Pred. No. 1.1e-45;
0; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT PAPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-03-16
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR PILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR PILING DATE: 1992-05-07
PRIOR PILING DATE: 1992-05-07
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1992-06-07
PRIOR FILING DATE: 1991-08-14
NUMBER: OF SEQ ID NOS: 64
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Best Local Similarity 97.2%;
Matches 106; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-08-466-163B-1
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115 PAPEMLGGPSVFIFPPKPKDTLLIARTPEVTCVVVDLGPEDPEVQISWF-VDGKQMQTAK 173
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                                                                                                                                                                                                                                                                              Query Match 27.6%; Score 512; DB 2; Length 334; Best Local Similarity 35.9%; Pred. No. 2.1e-41; Matches 123; Conservative 60; Mismatches 122; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 FLYSKLSVDKSRWQRGDTFICAVWHEALHNHYT-QKSLSHSPG 333
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Fatent No. 5994514
GENERAL INFORMATION:
TITLE OF INVENTION: IMMUNOGLOBULIN VARIANTS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STREET: 1 USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,025A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-Jun-1995
N: 530
                              1488-106
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SYOBOGA, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET UNMBER: P0718
TELEDOMAUNICATION INFORMATION:
TELEPHONE: 650/225-1489
     32,181
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                       LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881
FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              ) TOPOLOGY: linear
) MOLECULE TYPE: peptide
US-08-646-981-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
US-08-464-025A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-646-981-16

Sequence 16, Application US/08646981

Sequence 16, Application US/08646981

Sequence 16, Application US/08646981

Sequence 16, Application US/08646981

SEPLICANT: MAEDA, YASUVUKI

APPLICANT: EDA, YASUVUKI

APPLICANT: ONO, YOICH

APPLICANT: ONO, YOICH

APPLICANT: ONO, YOICH

APPLICANT: ONO, YOICH

APPLICANT: ONO, YOICH

APPLICANT: ONO, YOICH

APPLICANT: ONO, YOICH

APPLICANT: ONO, YOICH

TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE

TITLE OF INVENTION: FRAGMENT CODING

TITLE OF INVENTION: FRAGMENT

CORRESPONDENCE ADDRESS:

ADDRESSER: BIRCH, STEWART, KOLASCH AND BIRCH

STREET: PO BOX 747

CITY: FALLS CHURCH

STATE: VA

COUNTRY: USA

COUNTRY: USA

ZIP: Z2040-0747

COMPUTER: TBM PC Compatible

OOREMATING SYSTEM: PC-DOS/MS-OS

SOFTWARE: PATENTIN RELABBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OOREMATING SYSTEM: PC-DOS/MS-OS

SOFTWARE PATENTIN RELABBLE FORM:

MEDIUM TYPE: PLOPPY DISK

CONFUTER: DATE OF DATA:

APPLICATION NUMBER: US/08/646,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.0%; Score 538; DB 2; Length 106; 98.1%; Pred. No. 1.1e-44; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 GTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPG 232
        MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                         OPERATING SYSTEM: PC-DUS/MB-LOC

SOFTWARE: Witheatin (Genettech)

CURRENT APPLICATION NUMBER: US/08/232,539D

FILING DATE: 21-Apr-1994

CLASSIFICATION: 21-Apr-1994

CLASSIFICATION: 28/178583

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/178583

FILING DATE: 07-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/744768

FILING DATE: 14-AuG-1991

APPLICATION NUMBER: 39,044

FILING DATE: 14-AuG-1991

ATTORNEY/AGENT INFORMATION:

NAME: SOODOMA: Craig G.

REGISTRATION NUMBER: 39,014

REFERENCE/DOCKET NUMBER: 90718P3

TELEFONE: 650/252-1489

TELEFONE: 650/252-1489

TELEFAX: 650/252-1489

TELEFAX: 650/252-1489

TELEFAX: 650/252-1489

TELEFAX: 650/252-1489

TELEFAX: 650/252-1489

TELEFAX: Amino acids

TYPE: Amino Acid

TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 29.0
Best Local Similarity 98.1
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
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188 NGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPE 247
                                                                                                                                 B--TGTTRIVICLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFFLYSRML 305
                                                                                                                                                                                                                             238 ELSSSDTVTLTCLIKDFFPPEIDVEWQSNGQPEPESKYHTTAPQLDE--DGSYFLYSKLS 295
          130 VSAYLSRPSPFDLF-IRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHS-TRKEEKQR 187
                                                                                                                                                                                                                                                                                               306 VNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
                                                                                                                                                                                                                                                                                                                              US-08-466-151-1
Sequence 1, Application US/08466151
Patent No. 603/453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESSENDENCE ADRRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DAR WAY
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIF: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P0718P2C1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PRING DATE:
PRING DATE:
PRIOR APPLICATION:
PROBLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-Jun-1995
FILING DATE: 06-Jun-1995
PRIOR APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07/8741992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/44768
FILING DATE: 14-AUG-1991
APTICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: SVODGA, CTALG G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: POT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39,044
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TELEFAX: 650/922-9881
INFORMATION FOR SEQ ID 00: 1:
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 118 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Svoboda, Craig G. REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-466-151-1
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                                                                                                                                                                                                                   124 DSNPRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRAS----GKPVNHS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 -LYSLSSMVIVPSSR-LPSETFICNVVHPATNTKVDKPGVPKESTCKCISPCPVPESLGG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 QTFSLQSEVNITQGQMMSSNTYTCHVKHNGS-----IFEDSSRKCADSNP----RG 129
                                                                                                                                                                                                                                                              2 DSNPRGVSAYLSRPSPFDXLFIRKSPTITCLVVDLAPSKGTVNLTWSRXASXXGKPVNHS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                              180 TRKEEKQR----NGTLIVTSTLPVGTRDWIEGETYQCRVTHPHLPRAL-MRSTTKLPG 232
                                                                                                                                                                                                                                                                                                                                          TRKEEKQRXNXXGTLIVUTSTLPVGTRDWIEGETYQCRVTHPHLPRALXWRSTTKTSG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 PTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTWLVDGQEAENLFPYTTRPKREGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 PSVFPLAPSCG--STSGSTVTLACLVSGYFPEPVTVSW-NSGSLTSGVHTFPSVLKSSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: EACH, MACHI, KAZUHIKO
APPLICANT: KIMACHI, KAZUHIKO
APPLICANT: EDA, YASUUKI
APPLICANT: ONO, YOICHI
APPLICANT: ONLYOSHI, SACHIO
TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
TITLE OF INVENTION: PRAGMENT CODING FOR CONSTANT REGION OF CANINE
NUMBER OF SEQUENCES: IMMUNOGLOBULINS
NUMBER OF SEQUENCES: STEELY, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
27.0%; Score 501.5; DB 2; Length 331;
Best Local Similarity 36.3%; Pred. No. 2.2e-40;
Matches 122; Conservative 62; Mismatches 125; Indels 27.
                                                                                                                       27.4%; Score 508; DB 2; Length 119; llarity 88.9%; Pred. No. 1.1e-41; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/08646981
Patent No. 5852183
PAPELICANT: MAEDA, HIROAKI
APPLICANT: EDA, YASUVUKI
APPLICANT: KIMACHI, KAZUHIKO
APPLICANT: ONO, YOICHI
APPLICANT: TOKIYOSHI, SACHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 14
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
                                           ; TOPOLOGY: Linear
US-08-464-025A-1
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Best Local Similarity
                                                                                                                                         Similarity
                                                                                                                                                                  104;
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Best Local (
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Matches
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Gaps
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    Length 118;
                                            Indels
Query Match 26.4%; Score 490.5; DB 3; Best Local Similarity 88.0%; Pred. No. 5.5e-40; Matches 103; Conservative 1; Mismatches 4;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKEEKQRNGTLIVISTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPK 78
DSNPRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRAS---GKPVNHS 179
                                                 TRKEEKQR----NGTLTUTSTLPVGTRDWIEGETYQCRVTHPHLPRAL-MRSTTKLPG 232
                                                               4 PSVFPLAPSCGTTSGA--TVALACLVLGYFPEPVTVSWNSGALTSG---VHTFPAVL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP----RGVSAYLSRPSPFD-LFIRKSPITICLVVDLAPSKGTVNLTWSRASGKPVNHST
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 REGGGTFSLQSEVNITQGQWMSSNTYTCHVKH - NGSIFEDSSRK-
                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ed. No. 2.9e-39;
Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 490; DB 1;
Pred. No. 2.9e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-UN-1995
CLASSIPICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 341255/1992
FILING DATE: 28-NOV-1992
ATTORNEY AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/POCKET NUMBER: KIMACHI=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTA RELEASE #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,463
FILING DATE: 26-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                   ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 34.28
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-436-463-6
                                                                                                                                 US-08-436-463-6
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  124
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4 PSVFPLAPSCGTTSGA--TVALACLVLGYFPEPVTVSWNSGALTSG---VHTFPAVL---
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                                                                            241 MLPPSPEETGTTR-TVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFF
                                                                                                             APPLICANT: ALEAN, HIVOTO APPLICANT: MAEDA, HIVOTO APPLICANT: MAEDA, HIVOTO APPLICANT: NIGHTYAMA, KIYOTO APPLICANT: NIGHTYAMA, KIYOTO APPLICANT: TOKIYOSHI, Sachio APPLICANT: TOKIYOSHI, Sachio APPLICANT: TOHYA, YUKINOBHI TAKESHI TAKESHI TALE OF INVENTION: ANTI-FELINE CALCIVIRUS RECOMBINANT TITLE OF INVENTION: ANTIBODY AND GENE FRACMENT ENCODING THE SAME NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: MECNER, CANTOR, MUELLER & PLAYER STREET: 1233 20th Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
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26.4%; Score 490; DB 1; Length 333;
Best Local Similarity 34.2%; Pred. No. 2.9e-39;
Matches 117; Conservative 63; Mismatches 126; Indels
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                                                                                                                                                                                                                      292 VYSKLSVDRSHWQRGNTYTCSVSHEALHSHHT-QKSLTQSPG 332
                                                                                                                                                                                     300 LYSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/024,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 24,392
REFERENCE/DOCKET NUMBER: P-500-23744
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFFLICATION UNDERS.
FILING DATE: 19930301
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 79189/1992
FILING DATE: 28 FEB-1992
ATTORNEY AGENT INFORMATION:
NAME: CANTOR, Herbert I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 20036-8218
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk'.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 6, Application US/08024253; Patent No. 5785968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 333 amin
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuhiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (202) 887-0400
(202) 835-0605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-08-024-253-6
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                   114 PPPEMLGGPSIFIFPPKPKDTLSISRTPEVTCLVVDLGPDDSDVQITWFVDNTQVYTAKT 173
                                                                                                                                   MLPPSPEETGTTR-TVTCLIRGFYPSEISVQWLFNNEEDHTGHHTTTRPQKDHGTDPSFF 299
                                                                                                                                                      71 FPYTTRPKREGGQTFSLQSEVNITQGQWMSSNTYTCHVKHNGSIFEDSSRKCADSNP--- 127
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                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09313942

Patent No. 6472179

GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: ADD USING
TITLE OF INVENTION: ADD USING
TITLE OF INVENTION: ADD USING
TITLE OF INVENTION: ADD USING
FILE REPERENCE: REG 203-A
CURRENT APPLICATION NUMBER: 09/313,942

PRIOR APPLICATION NUMBER: 09/313,942

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 32

SEQ ID NOS: 32

SEQ ID NO 12

LINGTH: 329
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                                                                 181 RKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVY
                                                                                      126 NP----RGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----RGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 STRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 SGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 FFLYSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAG 341
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                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-09-313-942-12
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RESULT 13 US-08-71-277A-47 Sequence 47, Application US/08761277A, Parent No. 5972334

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69 VIVPSSS-LGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKP 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 LVKGFYPSDIAVEWESNGQPEN--NYKTTPPVLD--SDGSFFLYSRLTVDKSRWQBGNVF 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 FD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 RSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG---VHTFPAVL----QSSGLYSLSSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
APPLICANT: Denney Jr., Dan W.
TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
TITLE OF INVENTION: Leukemia
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.6%; Score 476; DB 2; Length 32 Best Local Similarity 35.8%; Pred. No. 6.5e-38; Matches 116; Conservative 57; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
FILING DATE: 06-DBC-1996
CLASSIFICATION NUMBER: US 08/644,664
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MacKhight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFENENCE/DOCKET NUMBER: GENITOPE-02406
TELECHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION: CREATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 SCSVMHEALHNHYT-QKSLSLSLG 326
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US-08-656-586-9
; Sequence 9, Application US/08656586
; Patent No. 5834597
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-761-277A-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-LFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRGEYPSEISVOWLENNEEDHTGHHTTTRPOKDHGTDPSFFLYSRMLVNKSIWEKGNLVT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 VKGFYPSDIAVEWESNGQPEN--NYKITPPMLD--SDGSFFLYSKLTVDKSKWQQGNVFS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 RSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG---VHTFPAVL----QSSGLXSLSSV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 RGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRPKREGGQTFSLQSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 GTRDWIEGETYQCRYTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPEB-TGTTRTVTCL
                                                and
APPLICANT: Tso, J. Yun
APPLICANT: Cole, Michael S.
APPLICANT: Cole, Michael S.
APPLICANT: Anaseti, Claudio
TITLE OF INVENTION: Mutated No. 5834597activating IgG2 Domains of TITLE OF INVENTION: Anti-CD3 Antibodies Incorporating the Same NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.6%; Score 475.5; DB 2; Length 326; llarity 35.8%; Pred. No. 7.2e-38; Conservative 57; Mismatches 120; Indels 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "heavy chain constant region of IgG2 mutant 3"
                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUBER: US/08/656,586 FILING DATE: 31-MAY-1996 CLASSIFICATION: 530
                                                                   11823-007210US
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: CLASSO ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O. REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-0(
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 576-0200
TELEPRAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRVVHEALPGSRTLEKSLHYS 339
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 326 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..326
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Protein
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Best Local Similarity
Matches 115; Conserv
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                                                               APPLICANT: Garin-Cheas, Pilar
APPLICANT: Garin-Cheas, Pilar
APPLICANT: Garin-Cheas, Pilar
APPLICANT: Leger, Uwe
APPLICANT: Leger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
APPLICANT: Rettig, Wolfgang J.
APPLICANT: Rettig, Wolfgang J.
APPLICANT: Rettig, Wolfgang J.
APPLICANT: Rettig, Wolfgang J.
APPLICANT: Rettig, Wolfgang J.
APPLICANT: Rettig, Wolfgang J.
APPLICANT: PILING PATE: 1999-04-29
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT PILING DATE: 1999-04-30
EARLIER PILING DATE: 1999-04-30
SALIER PILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
STORTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 PPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW----LVDGQEAENLFPYTTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 PSVFPLAPSSKSTSG---GTAALGCLVKDYFPEPVTVSWNSGALTSG---VHTFPAVL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.6%; Score 457; DB 4; Length 330; 34.7%; Pred. No. 4.6e-36;
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ne : 25 secs
Sequence 22, Application US/09301593A
Patent No. 6455677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 34.7%
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-09-301-593-22
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